

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 20, 2005, 15:14:10 ; Search time 75 Seconds
(without alignments)
2346.346 Million cell updates/sec

Title: US-10-622-201-70

Perfect score: 2288

Sequence: 1 MLHGASRRPARKSSGLSG.....FMDIAGLGAKIELSDTKAA 455

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2288	100.0	455	2	AAR26449 CP4-EPSPS
2	2288	100.0	455	2	AAW39426 CP4-EPSPS
3	2288	100.0	455	7	AAE39920 Class II
4	2288	100.0	455	8	ADJ79608 A_tumefac
5	2288	100.0	527	4	AAW52214 EPSPS SEQ
6	2282	99.7	455	2	AAR22300 Class II
7	2282	99.7	455	2	AAW24683 Class II
8	2282	99.7	455	2	AAW24474 Class II
9	2282	99.7	455	2	AAW71609 Agrobacte
10	2282	99.7	455	4	AAE05053 Agrobacte
11	2282	99.7	455	6	AAE31621 5-Enolpyr
12	2282	99.7	455	7	AAE39899 Agrobacte
13	1900.5	83.1	449	2	AAR22301 Class II
14	1900.5	83.1	449	2	AAR22302 Class II
15	1900.5	83.1	449	2	AAW34685 Class II
16	1900.5	83.1	449	2	AAW34684 Class II
17	1900.5	83.1	449	2	AAW34680 Class II
18	1900.5	83.1	449	2	AAW24479 Class II
19	1900.5	83.1	449	2	AAW71611 Pseudomon
20	1900.5	83.1	449	2	AAW71610 Pseudomon
21	1900.5	83.1	449	4	AAE05055 Pseudomon
22	1900.5	83.1	449	4	AAE05054 Pseudomon
23	1900.5	83.1	449	7	AAE39900 Agrobacte
24	1900.5	83.1	449	7	AAE39901 Pseudomon
25	1783	77.9	452	8	ADS23083 Bacterial

26	1233.5	53.9	430	8	ADS42336 Bacterial
27	1213.5	53.0	432	8	ADS21443 Bacterial
28	1189.5	51.9	418	8	ADN25161 Bacterial
29	1149.5	50.2	420	8	ADS29006 Bacterial
30	1135	49.6	443	8	ADS28041 Bacterial
31	989.5	43.2	782	7	ABO72808 Pseudomon
32	983	43.0	411	8	ADN27321 Bacterial
33	961.5	42.0	758	6	ADA33234 Acinetoba
34	927.5	40.5	442	8	ADS26350 Bacterial
35	912.5	39.9	454	8	ADS28697 Bacterial
36	908.5	39.7	408	8	ADN26649 Bacterial
37	908.5	39.7	412	8	ADN26846 Bacterial
38	906.5	39.6	408	8	ADS26718 Bacterial
39	906.5	39.6	408	8	ADS27102 Bacterial
40	902.5	39.4	773	8	ADL05904 M. catarr
41	884	38.6	431	8	ADS28209 Bacterial
42	878	38.4	675	8	ADS24901 Bacterial
43	867.5	37.9	447	2	AAW34688 Class II
44	867.5	37.9	447	2	AAW24487 Class II
45	867.5	37.9	447	2	AAW71619 Synechocy

ALIGNMENTS

RESULT 1
AAR26449
ID AAR26449 standard; protein, 455 AA.
XX
AC AAR26449;
XX
DT 25-MAR-2003 (revised)
DT 28-JAN-1993 (first entry)
XX
XX CP4-EPSPS.
XX
XX PMON11030; CTP2; CP4; EPSPS; chloroplast transit peptide;
XX 5-enolpyruvyl-3-shikimate phosphate synthetase; Acc; ethylene;
XX Pseudomonas chloraphis 6G5.
XX
OS Synthetic.
XX
XX W09212249-A1.
XX
PD 23-JUL-1992.
XX
PF 17-DEC-1991; 91WO-US009437.
XX
XX 26-DEC-1990; 90US-00632440.
XX
PA (MONS) MONSANTO CO.
XX
XX Klee HJ, Kishore GM;
XX
XX WPI; 1992-284334/34.
XX N-FSDB; AAQ27201.
XX
XX Delaying fruit ripening and senescence in plants - by controlling
XX ethylene@ prodn., pref. by expression of 1-amino-cyclopropane-1-
XX carboxylic acid deaminase.
XX
XX Disclosure; Page 64-66; 110pp; English.
XX
XX The sequences given in AAR26448 and AAR26449 are encoded by genes which
XX were used in the construction of an expression plasmid pMON11030 which
XX was used to transform petunia plants. This plasmid contained the genes
XX for chloroplast transit peptide (CTP2) (AAR26448) and the CP4 synthetic 5
XX -enolpyruvyl-3-shikimate phosphate synthetase (EPSPS) gene (AAR26449)
XX which is capable of conferring resistance to glyphosate. The plasmid also
XX contained the 1-aminocyclo-propane-1-carboxylic acid (ACC) deaminase gene
XX from Pseudomonas chloraphis (see also AAQ27199). The transformed plants
XX had ethylene levels reduced to about one half that of the control,
XX untransformed plants. It is expected that such plants will show reduced

CC sense of flowers and leaves when compared to untransformed plants.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 455 AA;

Query Match 100.0%; Score 2288; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.2e-180;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLHGASSRPATARKSSGSGTVRIIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60
 DB 1 MLHGASSRPATARKSSGSGTVRIIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60
 QY 61 KAMQMGARIRKEGDTWIIDGVNGGLAPAPLDFGNAATGCRITMGLVGYDPDSTFI 120
 DB 61 KAMQMGARIRKEGDTWIIDGVNGGLAPAPLDFGNAATGCRITMGLVGYDPDSTFI 120
 QY 121 GDASLTKEPMGRVNLPLREMGVOVKSSEDGRLPVTLRGPKTPTPTTYRVPMAAQAQVKSAY 180
 DB 121 GDASLTKEPMGRVNLPLREMGVOVKSSEDGRLPVTLRGPKTPTPTTYRVPMAAQAQVKSAY 180
 QY 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGSKLTGQVID 240
 DB 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGSKLTGQVID 240
 QY 241 VPGDSSSTAFPLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGSD 300
 DB 241 VPGDSSSTAFPLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGSD 300
 QY 301 VADLVRSSSTLKGTVVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLBELRVKESDRLSA 360
 DB 301 VADLVRSSSTLKGTVVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLBELRVKESDRLSA 360
 QY 361 VANGKLNGVDCDEGETSLVVRGPDGKGLGNASGAAVAATHLDRHIAMSFLVMGLVSENP 420
 DB 361 VANGKLNGVDCDEGETSLVVRGPDGKGLGNASGAAVAATHLDRHIAMSFLVMGLVSENP 420
 QY 421 VTVDATMTATSPPEFMDLMAGLAKIELSDTKAA 455
 DB 421 VTVDATMTATSPPEFMDLMAGLAKIELSDTKAA 455

RESULT 2

AAW39426
 ID AAW39426 standard; protein; 455 AA.

AC AAW39426;

DT 19-MAY-1998 (first entry)

DE CP4-EPSPS protein.

XX 1-aminocyclopropane-1-carboxylic acid deaminase; ACC deaminase;
 KW fruit ripening; ethylene production; glyphosate resistance;
 KM 5-enolpyruvyl-3-shikimate phosphate synthase; EPSPS; CP4.

OS Synthetic.

PN US5702933-A.

PD 30-DEC-1997.

PF 06-NOV-1995; 95US-00553943.

PR 26-DEC-1990; 90US-00632440.

PR 17-DEC-1991; 91US-00809457.

PA (MONS) MONSANTO CO.

PI Klee HJ, Kishore GM;

DR WPI: 1998-076419/07.

DR N-PSDB; AAV09719.

XX Production of plants with delayed ripening - using DNA encoding 1-
 PT amino:cyclo:propane-1-carboxylic acid deaminase.
 XX
 XX Example 9; Fig 21; 56pp; English.

CC This sequence represents the synthetic CP4 5-enolpyruvyl-3-shikimate
 CC phosphate synthase (EPSPS) gene which is capable of conferring resistance
 CC to glyphosate and is used in a novel method for producing fruit-bearing
 CC plants with delayed ripening. The method involves the expression of a 1-
 CC aminocyclopropane-1-carboxylic acid (ACC) deaminase gene in a plant at a
 CC level sufficient to reduce ethylene production in the fruit

XX Sequence 455 AA;

Query Match 100.0%; Score 2288; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.2e-180;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLHGASSRPATARKSSGSGTVRIIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60
 DB 1 MLHGASSRPATARKSSGSGTVRIIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60
 QY 61 KAMQMGARIRKEGDTWIIDGVNGGLAPAPLDFGNAATGCRITMGLVGYDPDSTFI 120
 DB 61 KAMQMGARIRKEGDTWIIDGVNGGLAPAPLDFGNAATGCRITMGLVGYDPDSTFI 120
 QY 121 GDASLTKEPMGRVNLPLREMGVOVKSSEDGRLPVTLRGPKTPTPTTYRVPMAAQAQVKSAY 180
 DB 121 GDASLTKEPMGRVNLPLREMGVOVKSSEDGRLPVTLRGPKTPTPTTYRVPMAAQAQVKSAY 180
 QY 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGSKLTGQVID 240
 DB 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGSKLTGQVID 240
 QY 241 VPGDSSSTAFPLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGSD 300
 DB 241 VPGDSSSTAFPLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGSD 300
 QY 301 VADLVRSSSTLKGTVVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLBELRVKESDRLSA 360
 DB 301 VADLVRSSSTLKGTVVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLBELRVKESDRLSA 360
 QY 361 VANGKLNGVDCDEGETSLVVRGPDGKGLGNASGAAVAATHLDRHIAMSFLVMGLVSENP 420
 DB 361 VANGKLNGVDCDEGETSLVVRGPDGKGLGNASGAAVAATHLDRHIAMSFLVMGLVSENP 420
 QY 421 VTVDATMTATSPPEFMDLMAGLAKIELSDTKAA 455
 DB 421 VTVDATMTATSPPEFMDLMAGLAKIELSDTKAA 455

RESULT 3

AAE39920
 ID AAE39920 standard; protein; 455 AA.

AC AAE39920;

DT 18-DEC-2003 (first entry)

DE Class II EPSPS enzyme related protein.

XX Glyphosate tolerant 5-enolpyruvylshikimate-3-phosphate synthase; enzyme;
 KW transgenic plant; transgenic; herbicide; weed control; EPSPS.

OS Unidentified.

PN US2002168680-A1.

PD 14-NOV-2002.

PF 16-DEC-1999; 99US-00464099.

PR 31-AUG-1990; 90US-00576537.
 PR 28-AUG-1991; 91US-00749611.
 PR 13-SEP-1994; 94US-00306063.
 PR 07-APR-1997; 97US-00833485.
 PR 20-AUG-1998; 98US-00137440.
 XX (BARR/) BARRY G F.
 PA (KISH/) KISHORE G M.
 PA (PADG/) PADGETTE S R.
 PA (STRL/) STRALLINGS W C.
 XX Barry GF, Kishore GM, Padgette SR, Stallings WC;
 PI WPI: 2003-719984/68.
 DR
 XX
 PT New 5-enolpyruvylshikimate-3-phosphate synthase DNA sequence useful for
 PT producing genetically transformed plants, and selectively controlling
 PT weeds in a field containing crop having planted crop seeds or plants.
 XX
 PS Disclosure; Page 82-83; 158pp; English.
 CC The invention relates to glyphosate tolerant 5-enolpyruvylshikimate-3
 CC phosphate synthase (EPSPS) enzymes and nucleic acid molecules encoding
 CC such enzymes. The invention is useful for producing genetically
 CC transformed plants which are tolerant to a glyphosate herbicide and for
 CC selectively controlling weeds in a field containing a crop having planted
 CC crop seeds or plants. The present sequence is a protein related to the
 CC invention
 CC
 XX Sequence 455 AA;
 SQ
 Query Match 100.0%; Score 2288; DB 7; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.2e-180;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLHGASSRPARARKSSGSLGTVRIPGDKSISHSRFMGSLAGETRTTGLLEGEDVINTG 60
 DB 1 MLHGASSRPARARKSSGSLGTVRIPGDKSISHSRFMGSLAGETRTTGLLEGEDVINTG 60
 QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNATGRLTMGLVGYVDFDSTFI 120
 DB 61 KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNATGRLTMGLVGYVDFDSTFI 120
 QY 121 GNASLTGRMGVNLPLREMGVOVXSEDDRLPVTLRGKPTPTITRYRPMASAOVKSAY 180
 DB 121 GNASLTGRMGVNLPLREMGVOVXSEDDRLPVTLRGKPTPTITRYRPMASAOVKSAY 180
 QY 181 LLAGNTPGITTVIIEIMTRDTEKMLQGFGANLTVETDADGVRTIRLGRGLTGQVID 240
 DB 181 LLAGNTPGITTVIIEIMTRDTEKMLQGFGANLTVETDADGVRTIRLGRGLTGQVID 240
 QY 241 VEGDESSITAPLVAALLVPGSDVTILNVLNMPRTGLIITLQMGADIEVINPRLAGGED 300
 DB 241 VEGDESSITAPLVAALLVPGSDVTILNVLNMPRTGLIITLQMGADIEVINPRLAGGED 300
 QY 301 VADLRVRSSTLKGVTVPEDRAPSMIDERYIILAVAAFAAGATYTMGLIELRYKESRSLA 360
 DB 301 VADLRVRSSTLKGVTVPEDRAPSMIDERYIILAVAAFAAGATYTMGLIELRYKESRSLA 360
 QY 361 VANGKLKLVNVDCEGETSLVVRGPRPGKIGNAGAAVATLHDRIAMSFVWGLVSENP 420
 DB 361 VANGKLKLVNVDCEGETSLVVRGPRPGKIGNAGAAVATLHDRIAMSFVWGLVSENP 420
 QY 421 VTVDATMTIATSPFPEMDLMAIGAKIELSDTKAA 455
 DB 421 VTVDATMTIATSPFPEMDLMAIGAKIELSDTKAA 455
 RESULT 4
 ADJ79608 standard; protein; 455 AA.
 XX
 AC ADJ79608;

XX 06-MAY-2004 (first entry)
 DT
 XX
 XX A_tumefaciens EPSPS protein modified to be glyphosate resistant Segid15.
 DE
 XX
 XX EPSPS; glyphosate resistant; enolpyruvyl-3-phosphoshikimate synthase;
 KW transgene silencing; transgenic; plant; agronomical phenotype;
 KW drought tolerance; cold tolerance; herbicide tolerance; yield;
 KW disease resistance; insect resistance; genetic engineering.
 XX
 OS Agrobacterium tumefaciens.
 OS Synthetic.
 XX
 PN WO2004009761-A2.
 XX
 PD 29-JAN-2004.
 XX
 PF 10-JUL-2003; 2003WO-US021551.
 XX
 PR 18-JUL-2002; 2002US-0396665P.
 XX
 PA (MONS) MONSANTO TECHNOLOGY LLC.
 PI Plasinski S;
 XX
 DR WPI: 2004-132939/13.
 DR N-PSDB; ADJ79609, ADJ79610, ADJ79611, ADJ79616.
 XX
 PT Producing transgene silencing with artificial polynucleotides, useful in
 PT producing commercial transgenic plants having increased herbicide
 PT tolerance, insect resistance, drought tolerance, cold tolerance and
 PT disease resistance.
 XX
 PS Example 4; SEQ ID NO 15; 162pp; English.
 XX
 CC This invention relates to novel methods for constructing artificial
 CC polynucleotides and ways to reduce transgene silencing in transgenic
 CC plants. Specifically, it refers to introducing an artificial
 CC polynucleotide that is divergent from an endogenous plant gene, but which
 CC encodes a substantially identical protein. The present invention
 CC describes artificial polynucleotides that encode proteins with an
 CC agronomically useful phenotype, such as drought, cold or herbicide
 CC tolerance, increased yield and disease or insect resistance. In
 CC particular, it refers to a modified enolpyruvyl-3-phosphoshikimate
 CC synthase (EPSPS) enzyme required for the synthesis of aromatic amino
 CC acids, which is resistant to the phytotoxic herbicide glyphosate.
 CC Accordingly, these methods and compositions are useful for plant genetic
 CC engineering to produce commercially viable transgenic plants with
 CC improved agronomical phenotypes. This polypeptide sequence is an
 CC agrobacterium tumefaciens strain CP4 EPSPS protein modified to be
 CC glyphosate resistant with chloroplast transit peptide, given in an
 CC exemplification of the invention.
 CC
 XX Sequence 455 AA;
 SQ
 Query Match 100.0%; Score 2288; DB 8; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.2e-180;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLHGASSRPARARKSSGSLGTVRIPGDKSISHSRFMGSLAGETRTTGLLEGEDVINTG 60
 DB 1 MLHGASSRPARARKSSGSLGTVRIPGDKSISHSRFMGSLAGETRTTGLLEGEDVINTG 60
 QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNATGRLTMGLVGYVDFDSTFI 120
 DB 61 KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNATGRLTMGLVGYVDFDSTFI 120
 QY 121 GNASLTGRMGVNLPLREMGVOVXSEDDRLPVTLRGKPTPTITRYRPMASAOVKSAY 180
 DB 121 GNASLTGRMGVNLPLREMGVOVXSEDDRLPVTLRGKPTPTITRYRPMASAOVKSAY 180
 QY 181 LLAGNTPGITTVIIEIMTRDTEKMLQGFGANLTVETDADGVRTIRLGRGLTGQVID 240
 DB 181 LLAGNTPGITTVIIEIMTRDTEKMLQGFGANLTVETDADGVRTIRLGRGLTGQVID 240

Db 181 LLAGNTPGITTVIEPIRDRHTEKMLQGFGANLTVETDADGVRTIRLEGKLTGVYID 240
QY 241 VPGDPSSTAFPLVALLVPGSDVTILNVLMNPTRTGLITLTQEMGADIEVINPRLAGGED 300
Db 241 VPGDPSSTAFPLVALLVPGSDVTILNVLMNPTRTGLITLTQEMGADIEVINPRLAGGED 300
QY 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYLLAVAAAFAGATVMNGLEELRYKESDRISA 360
Db 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYLLAVAAAFAGATVMNGLEELRYKESDRISA 360
QY 361 VANGKLNGVDCDEBETSLVVRGRPDGKGLGNASGAAVATHLDRHRIANSFLVMGLVSENP 420
Db 361 VANGKLNGVDCDEBETSLVVRGRPDGKGLGNASGAAVATHLDRHRIANSFLVMGLVSENP 420
QY 421 VTVDATMIATISFPEFMDLMAGLGAKEISDTKAA 455
Db 421 VTVDATMIATISFPEFMDLMAGLGAKEISDTKAA 455

RESULT 5

AAMS2214
ID AAMS2214 standard; protein; 527 AA.

AC AAMS2214;

DT 11-SEP-2003 (revised)
DT 12-FEB-2002 (first entry)

DE EPSPS SEQ ID NO 3.

XX Transgenic plant; herbicide resistance; EPSPS; GOX; Petunia hybrida.
KM 5-enolpyruvylshikimate-3-phosphate synthase; glyphosate oxidoreductase;
KW protoporphyrinogen IX oxidase; immunoglobulin; Agrobacterium; strain CP4;
XX chloroplast transit peptide.

OS Petunia x hybrida.
OS Agrobacterium sp.

PN JP2001190168-A.

XX 17-JUL-2001.

PF 27-OCT-2000; 2000JP-00328811.

PR 29-OCT-1999; 99JP-00310244.

PA (SUMO) SUMITOMO CHEM CO LTD.

DR WPI; 2001-605307/69.

DR N-PSDB; ABR02854.

XX New herbicide-resistant plant.

PS Example; Page 46-48; 66pp; Japanese.

XX The invention relates to a transgenic plant which shows resistance to a
CC herbicide in an amount inhibiting natural 5-enolpyruvylshikimate-3-
CC phosphate synthase (EPSPS) activity of the plant and having at least one
CC enzymatic activity selected from: (1) EPSPS activity different from
CC natural EPSPS activity of the plant or (2) glyphosate oxidoreductase
CC (GOX) activity different from the natural GOX activity of the plant; and
CC in which a gene encoding a protein having the following properties: (a)
CC combines specifically with a substance participating to the herbicidal
CC activity a herbicide of protoporphyrinogen IX oxidase inhibiting type;
CC (b) has substantially no denaturing activity on a substance to which said
CC protein combines specifically; and (c) contains substantially no
CC framework region of the variable region of immunoglobulin. The present
CC sequence is that of the Petunia hybrida EPSPS chloroplast transit peptide
CC and the Agrobacterium sp. strain CP4 EPSPS gene. (Updated on 11-SEP-2003
CC to standardise OS field)

XX Sequence 527 AA;

Query Match 100.0%; Score 2288; DB 4; Length 527;
Best Local Similarity 100.0%; Pred. No. 1,4e-180;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLHGSSRPATARKSSGSGVTRIPGDSISHSRFMFGLASGETRTGLLEGEDVINTG 60
Db 73 MLHGSSRPATARKSSGSGVTRIPGDSISHSRFMFGLASGETRTGLLEGEDVINTG 132
QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLLAPAPLDFGNAATGCRITMGLVGVDSTFI 120
Db 133 KAMQAMGARIRKEGDTWIIDGVNGGLLAPAPLDFGNAATGCRITMGLVGVDSTFI 192
QY 121 GDASTTKPMKRVNPLREMGVQVSEBGRDLPYTLRCKPTPTPTTYVPMAAQAQKSAV 180
Db 193 GDASTTKPMKRVNPLREMGVQVSEBGRDLPYTLRCKPTPTPTTYVPMAAQAQKSAV 252
QY 181 LLAGNTPGITTVIEPIRDRHTEKMLQGFGANLTVETDADGVRTIRLEGKLTGVYID 240
Db 253 LLAGNTPGITTVIEPIRDRHTEKMLQGFGANLTVETDADGVRTIRLEGKLTGVYID 312
QY 241 VPGDPSSTAFPLVALLVPGSDVTILNVLMNPTRTGLITLTQEMGADIEVINPRLAGGED 300
Db 313 VPGDPSSTAFPLVALLVPGSDVTILNVLMNPTRTGLITLTQEMGADIEVINPRLAGGED 372
QY 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYLLAVAAAFAGATVMNGLEELRYKESDRISA 360
Db 373 VADLRVRSSTLKGVTVPEDRAPSMIDEPYLLAVAAAFAGATVMNGLEELRYKESDRISA 432
QY 361 VANGKLNGVDCDEBETSLVVRGRPDGKGLGNASGAAVATHLDRHRIANSFLVMGLVSENP 420
Db 433 VANGKLNGVDCDEBETSLVVRGRPDGKGLGNASGAAVATHLDRHRIANSFLVMGLVSENP 492
QY 421 VTVDATMIATISFPEFMDLMAGLGAKEISDTKAA 455
Db 493 VTVDATMIATISFPEFMDLMAGLGAKEISDTKAA 527

RESULT 6

AAR22300
ID AAR22300 standard; protein; 455 AA.

XX AAR22300;

DT 24-OCT-2003 (revised)
DT 03-AUG-1992 (first entry)

DE Claes II EPSPS enzyme.

KM Glyphosate tolerant bacteria; herbicides; glyphosate resistant plants;
KW 5'-enolpyruvylshikimate-3-phosphate synthase; weed control.

OS Agrobacterium sp; strain CP4.

PN WO9204449-A.

XX 19-MAR-1992.

PF 28-AUG-1991; 91WO-US006148.

PR 31-AUG-1990; 90US-00576537.

PA (MONS) MONSANTO CO.

DR Barry GF, Kishore GM, Padgett SR;

DR WPI; 1992-114356/14.

XX DNA encoding Claes II 5'-enolpyruvyl shikimate-3-phosphate synthase - for
XX producing plants and bacteria tolerant to glyphosate herbicides.

XX Disclosure; Fig 3; 148pp; English.

XX The sequence is that of the Class II 5'-enolpyruvylshikimate-3 phosphate


```
OY 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYITLVAFAAGATVMNGLEELRYKESDRLSA 360
DB 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYITLVAFAAGATVMNGLEELRYKESDRLSA 360
OY 361 VANGIKLNGVDCDEGETSLVVRGPRDGKGLGNASGAAVATHLDHRIAMSLVMGLVSENP 420
DB 361 VANGIKLNGVDCDEGETSLVVRGPRDGKGLGNASGAAVATHLDHRIAMSLVMGLVSENP 420
OY 421 VTVDATMIATSFPEFMDLMAGLGAKIELSDTKAA 455
DB 421 VTVDATMIATSFPEFMDLMAGLGAKIELSDTKAA 455

RESULT 8
AAW24474
ID AAW24474 standard; protein; 455 AA.
AC AAW24474;
XX
XX 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 02-OCT-1997 (first entry)
XX
DE Class II EPSPS for glyphosate resistant plant production.
KM 5-enolpyruvylshikimate-3-phosphate synthase; EPSPS; Class II;
KM glyphosate resistant; transgenic plant; herbicide; shikimic acid;
KM fusion protein; soybean; corn; wheat; barley; cotton; sugarbeet; tobacco.
XX
OS Agrobacterium sp; strain CP4.
XX
XX US5633435-A.
XX
XX 27-MAY-1997.
XX
XX 13-SEP-1994; 94US-00306063.
XX
XX 31-AUG-1990; 90US-00576537.
XX 28-AUG-1991; 91US-00749611.
XX
XX (MONS ) MONSANTO CO.
XX
XX Padgette SR, Stallings WC, Barry GF, Kishore GM;
XX
XX WPI; 1997-297418/27.
XX
XX N-PSDB; AAT77313.
XX
XX New isolated 5-enol:pyruvyl:shikimate-3-phosphate synthase gene - used
XX for transforming plants to produce plants which are tolerant to
XX glyphosate herbicide.
XX
XX Claim 1; Col 57-60; 154pp; English.
XX
XX AAW24474 shows the sequence of a class II 5-enolpyruvylshikimate-3-
XX phosphate synthase (EPSPS) enzyme. Class II EPSPS enzymes are tolerant to
XX glyphosate herbicides. EPSPS and sequences encoding it are used for the
XX production of herbicide resistant (glyphosate-tolerant) plants such as
XX corn, wheat, rice, barley, soybean, cotton, sugarbeet, oilseed rape,
XX canola, flax, sunflower, potato, tobacco, tomato, alfalfa, poplar, pine,
XX eucalyptus, apple, lettuce, peas, lentils, grape and turf grasses.
XX (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to
XX standardise OS field)
XX
XX Sequence 455 AA;
XX
XX Query Match 99.7%; Score 2282; DB 2; Length 455;
XX Best Local Similarity 99.8%; Pred. No. 3, 6e-180;
XX Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 MLHGASSRPATARKSSGSLGTVRIPDGKISHRSFWMFGGLASGETPTTGLSGEDVYNTNG 60
DB 1 MSHGASSRPATARKSSGSLGTVRIPDGKISHRSFWMFGGLASGETPTTGLSGEDVYNTNG 60
```

```
OY 61 KAMQAMGARIRKEGDTWIIIDGVNGGLIAPAPLDFGNAATGCRITMGLVGVYDFDSTFI 120
DB 61 KAMQAMGARIRKEGDTWIIIDGVNGGLIAPAPLDFGNAATGCRITMGLVGVYDFDSTFI 120
OY 121 GDASLTKRPMGRVNLPLPEMGVQVKSIEDGRLPTLRGPKTPTPTTYVPMASAOVKSAY 180
DB 121 GDASLTKRPMGRVNLPLPEMGVQVKSIEDGRLPTLRGPKTPTPTTYVPMASAOVKSAY 180
OY 181 LLAGINTPGITTVTLEPIITRDRHTEKMLQFGANLIVETDADGVRTIRLEGKGLTGQYID 240
DB 181 LLAGINTPGITTVTLEPIITRDRHTEKMLQFGANLIVETDADGVRTIRLEGKGLTGQYID 240
OY 241 VPGDPSSTAFPLVAALVPGSDVTITLVNLPRTGILITTOEWGADIEVINPRLAGGED 300
DB 241 VPGDPSSTAFPLVAALVPGSDVTITLVNLPRTGILITTOEWGADIEVINPRLAGGED 300
OY 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYITLVAFAAGATVMNGLEELRYKESDRLSA 360
DB 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYITLVAFAAGATVMNGLEELRYKESDRLSA 360
OY 361 VANGIKLNGVDCDEGETSLVVRGPRDGKGLGNASGAAVATHLDHRIAMSLVMGLVSENP 420
DB 361 VANGIKLNGVDCDEGETSLVVRGPRDGKGLGNASGAAVATHLDHRIAMSLVMGLVSENP 420
OY 421 VTVDATMIATSFPEFMDLMAGLGAKIELSDTKAA 455
DB 421 VTVDATMIATSFPEFMDLMAGLGAKIELSDTKAA 455

RESULT 9
AAW71609
ID AAW71609 standard; protein; 455 AA.
XX
XX AAW71609;
XX
XX 14-DEC-1998 (first entry)
XX
XX Agrobacterium sp. strain CP4 Class II EPSPS.
XX
XX 5-enolpyruvylshikimate-3-phosphate synthase; class II EPSPS enzyme;
XX glyphosate herbicide; transformed bacteria; class I EPSPS enzyme;
XX resistance; inhibition; 5-enolpyruvyl-3-phosphoshikimic acid;
XX N-phosphonomethylglycine.
XX
XX Agrobacterium sp.
XX
XX US5804425-A.
XX
XX 08-SEP-1998.
XX
XX 07-APR-1997; 97US-00833485.
XX
XX 31-AUG-1990; 90US-00576537.
XX 28-AUG-1991; 91US-00749611.
XX 13-SEP-1994; 94US-00306063.
XX
XX (MONS ) MONSANTO CO.
XX
XX Stallings WC, Padgette SR, Barry GF, Kishore GM;
XX
XX WPI; 1998-505657/43.
XX
XX N-PSDB; AAV58009.
XX
XX Glyphosate resistant 5-enol:pyruvyl:shikimate-3-phosphate synthase -
XX useful for characterisation of the enzyme to determine inhibition data
XX values.
XX
XX Claim 3; Fig 3; 152pp; English.
XX
XX An isolated 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) has the
XX sequence domains (I), (II), (III) and (IV): -R-X1-H-X2-E- (I), -G-D-K-X3-
XX (II); -S-A-Q-X4-R- (III); and -N-X5-T-R- (IV). Where X1 = G, S, T, C, Y,
```

N, O, D, R, E, X2 and X3 = S or T, X4 and X5 = A, R, N, D, C, O, E, G, H, I, L, K, M, F, P, S, T, W, Y or V. The BPSs enzyme, produced by *CC* recombinant methods, can be used in kinetic studies to determine K_i and K_m values of the enzyme for its characteristic reaction. The enzyme is normally used for the production of 5-enolpyruvyl-3-phosphoshikimic acid in *CC* plants, and most forms of the enzyme are inhibited by N-phosphonomethylglycine ('glyphosate') herbicides. Inhibition data enables *CC* more accurate values of concentrations of herbicide to be used when growing the plant without being detrimental to it. This enables the plant to be grown in the presence of the herbicide, being used to inhibit the growth of undesired plants. The present sequence represents a Class II BPSs from bacterial isolate *Agrobacterium* sp. strain C4

SQ Sequence 455 AA;

Query Match	99.7%;	Score 2282;	DB 2;	Length 455;
-------------	--------	-------------	-------	-------------

```
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy	1	MHAGSRRATARKSSGSLGTVARIPGDSXISHRSPFMGSLASGSTRITGLLEGEDVINTG	60
Db	1	MSHGASRRATARKSSGSLGTVARIPGDSXISHRSPFMGSLASGSTRITGLLEGEDVINTG	60
Qy	61	KAMQAMGATIRREKGDWTIIDVGNGLLAPPEAPLDPCMAAGCULTMGLVGVDFDSFTI	120
Db	61	KAMQAMGATIRREKGDWTIIDVGNGLLAPPEAPLDPCMAAGCULTMGLVGVDFDSFTI	120
Qy	121	GDASLTKRPMGRVLNLRMGVQVASEBQDRLPYLRGPKPTPTITRVPMASQVNSAV	180
Db	121	GDASLTKRPMGRVLNLRMGVQVASEBQDRLPYLRGPKPTPTITRVPMASQVNSAV	180
Qy	181	LLAGLNTPGIITTVIEIEIMTRDHTKMLQGFGANLIVETDADGVRTIRLEGRGKLTGV	240
Db	181	LLAGLNTPGIITTVIEIEIMTRDHTKMLQGFGANLIVETDADGVRTIRLEGRGKLTGV	240
Qy	241	VPPDPSSTAPLVAALLVPGSDVTLTLANLMPTRTGLILTIQEBGADIEVINPPLAGGED	300
Db	241	VPPDPSSTAPLVAALLVPGSDVTLTLANLMPTRTGLILTIQEBGADIEVINPPLAGGED	300
Qy	301	VADLRVRSSTLKGVTVPEDRAPSMIDEPYILAAVAAPFEGATVWNGLEELRVKESDLSA	360
Db	301	VADLRVRSSTLKGVTVPEDRAPSMIDEPYILAAVAAPFEGATVWNGLEELRVKESDLSA	360
Qy	361	VANGKLINGVDCDEGETSLVVRGPDGKGLGNASGAAYATHLDRILAMSPILWGLVSENP	420
Db	361	VANGKLINGVDCDEGETSLVVRGPDGKGLGNASGAAYATHLDRILAMSPILWGLVSENP	420
Qy	421	VTVDDATMTATSPPEFMDIMAGLGIKIELSDPKAA	455
Db	421	VTVDDATMTATSPPEFMDIMAGLGIKIELSDPKAA	455

RESULT 10
AAE05053

ID	AAE05053	standard; protein; 455 AA.
----	----------	----------------------------

AC AAE05053 ;

DT	11-SEP-2003	(revised)
DT	10-SEP-2001	(first entry)

DE Agrobacterium sp. strain CP4.class II EPSPS protein

KM 5-enolpyruvylshikimate-3-phosphate synthase; EPSPS; glyphosate-transformed bacteria; transgenic plant; herbicide.

OS *Agrobacterium* sp.; CP4.

PN US6248876-B1

PD 19-JUN-2001.

PF 20-AUG-1998; 98US-00137440

XX	31-AUG-1990;	90US-00576537.
PR	28-AUG-1991;	91US-00749611.
PR	13-SEP-1994;	94US-00306063.
PR	07-APR-1997;	97US-00833485.

PA (MONS) MONSANTO CO.

PI Barry GF, Kishore GM, Padgett SR, Stallings WC.

DR WPI; 2001-407326/43.

XX

PT the presence of a target genomic DNA encoding a 5-enolpyruvylshikimate-3-

PS Claim 3; Fig 3; 152pp; English.

CC The present invention relates to a DNA probe capable of use in a
CC polymerase chain reaction for identifying the presence of a target
CC genomic DNA encoding 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS)
CC enzyme referred to as class II EPSPS enzyme which is tolerant to
CC glyphosate. EPSPS genes are useful in producing transformed bacteria and
CC transgenic plants which are tolerant to glyphosate herbicide. The probe
CC is useful for identifying the presence of a target genomic DNA encoding a
CC EPSPS enzyme. The present sequence is Agrobacterium sp. strain CP4 class
CC II EPSPS protein. Note: The present sequence, SED ID NO. 3 is stated as
CC amino acid sequence throughout the specification. However, it is referred
CC as probe in claim 1 of the specification. (Updated on 11-SEP-2003 to
CC standardise OS field)

SQ Sequence 455 AA,

Query Match 99.7%; Score 2282; DB 4; Length 455

Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MLHGASSRATARKSSGSLGTVIRIGDXSISRHSMPFGSLGSETRITGLLEGEDVINTG	60
Db	1	MSHGASSRATARKSSGSLGTVIRIGDXSISRHSMPFGSLGSETRITGLLEGEDVINTG	60
Qy	61	KAMQAMGARIRKREGDWTIIIDVGNGGLLAPEAPLDFGNAATGCRITMGLVGVDYDSTFI	120
Db	61	KAMQAMGARIRKREGDWTIIIDVGNGGLLAPEAPLDFGNAATGCRITMGLVGVDYDSTFI	120
Qy	121	GDASLITKRPMGVANDLRPMGVQVQSEEDGDRPLPULRBPKPTPTITRVPMASQVQSAV	180
Db	121	GDASLITKRPMGRVANDLRPMGVQVQSEEDGDRPLPULRBPKPTPTITRVPMASQVQSAV	180
Qy	181	LILAGLWPGITTVIEIRIMTRDTEKMLQGFQGANLIVETDADGVRTIRLEGRGKLTQGVID	240
Db	181	LILAGLWPGITTVIEIRIMTRDTEKMLQGFQGANLIVETDADGVRTIRLEGRGKLTQGVID	240
Qy	241	VPDPPSSIAFPIVAALIVPGSDVTILNLYANMPTRTGTLILTLOEWGADIEVINPRLAGGED	300
Db	241	VPDPPSSIAFPIVAALIVPGSDVTILNLYANMPTRTGTLILTLOEWGADIEVINPRLAGGED	300
Qy	301	VALARRSSATLKGWYMPEDRAPSMTIDEPYIILAVAAAFEGATWNNGLEELVYKSSDSLISA	360
Db	301	VALARRSSATLKGWYMPEDRAPSMTIDEPYIILAVAAAFEGATWNNGLEELVYKSSDSLISA	360
Qy	361	VANGKLINGVDCDEGETSLVWRGRDQKGLGNASGAAYATHLDHRIAMSFLVMGLVSENP	420
Db	361	VANGKLINGVDCDEGETSLVWRGRDQKGLGNASGAAYATHLDHRIAMSFLVMGLVSENP	420
Qy	421	VYVDDATMTATSPPEFMDLMAGLGAKIELSDPKAA	455
Db	421	VYVDDATMTATSPPEFMDLMAGLGAKIELSDPKAA	455

RESULT 11
AAE31621

ID AAE31621 standard; protein; 455 AA.
XX
AC AAE31621;
XX
DT 24-FEB-2003 (first entry)
XX
DE 5-Enolpyruvylshikimate-3-phosphate synthase (EPSPS).
XX
KM Agricultural; transgenic; phytopathogenic disease; infection; therapy;
herbicide; food process; 5-enolpyruvylshikimate-3-phosphate synthase;
EPSPS; enzyme.
XX
OS Unidentified.
XX WO200284250-A2.
XX
PD 24-OCT-2002.
XX
PF 17-APR-2002; 2002WO-US012014.
XX
PR 17-APR-2001; 2001US-0284273P.
PR 18-APR-2001; 2001US-0284713P.
XX
PA (FEMT-) FEMTOLINK BIOTECHNOLOGIES LLC.
PI Everett NP, Petell JK, Young SA;
XX
DR WPI; 2003-046937/04.
XX
PT Detecting or quantifying target proteins in complex biological samples,
PT comprises analyzing peptide fragments via mass spectrometry, where
PT detection of a signature peptide indicates the presence of the target
PT protein in the sample.
XX
PS Example 3; Fig 3B; 50pp; English.
XX
CC The invention relates to a method for detecting or quantifying target
CC proteins in complex biological samples, which involves analyzing peptide
CC fragments via mass spectrometry, where detection of a signature peptide
CC indicates the presence of the target protein in the sample. The method is
CC useful in detecting, quantifying or characterizing target proteins in
CC complex biological samples, e.g. plants, animals or microorganisms, by
CC employing mass spectrometry-based techniques. It can also be applied in
CC agricultural diagnostic analyses, such as detection of genetically
CC modified organisms for insect or herbicidal resistance, or in the
CC diagnosis of phytopathogenic disease or contamination in plants, soil,
CC liquids, solids and other samples from environmental sources. It may also
CC be used to monitor for targeted proteins in manufacturing food processes,
CC and in various clinical and diagnostic analyses, such as monitoring
CC infections and treatment in humans and animals. The present sequence is 5
CC -enolpyruvylshikimate-3-phosphate synthase (EPSPS) used to illustrate the
CC method of the invention
XX
SQ Sequence 455 AA;
Query Match 99.7%; Score 2282; DB 6; Length 455;
Best Local Similarity 99.8%; Pred. No. 3,6e-180;
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MHGASSRPATARKSSGLSVTRIPGDKISHSFMRFGGLASGERTITGLBEEDVING 60
DB 1 MHGASSRPATARKSSGLSVTRIPGDKISHSFMRFGGLASGERTITGLBEEDVING 60
QY 61 KAMQAMGARIRKEGDTWIIDVONGGLAPAPLDFGNATGCRITMGVGVDFDSTFI 120
DB 61 KAMQAMGARIRKEGDTWIIDVONGGLAPAPLDFGNATGCRITMGVGVDFDSTFI 120
QY 121 GNASLTKRPMGRVLPRLREMGVOVKSDEGDRPLVTLRGKPTPTPIYRVPMASQVKSAY 180
DB 121 GNASLTKRPMGRVLPRLREMGVOVKSDEGDRPLVTLRGKPTPTPIYRVPMASQVKSAY 180
QY 181 LLAGINTPGITTVIEIMTRDHTKMLQGFANLTETADAGRTIRLRGRLTGQVID 240
DB 181 LLAGINTPGITTVIEIMTRDHTKMLQGFANLTETADAGRTIRLRGRLTGQVID 240

DB 181 LLAGINTPGITTVIEIMTRDHTKMLQGFANLTETADAGRTIRLRGRLTGQVID 240
QY 241 VPGDSSSTAPFLVAALLVPGSDVTIILNTLMNPTRTGLITLQEMGADIEVINPRLAGGED 300
DB 241 VPGDSSSTAPFLVAALLVPGSDVTIILNTLMNPTRTGLITLQEMGADIEVINPRLAGGED 300
QY 301 VADLVRSSSTLKGTVVPPDRAPSMIDEYPIILAVAAFAEGATVWNGLEELVKESDRISA 360
DB 301 VADLVRSSSTLKGTVVPPDRAPSMIDEYPIILAVAAFAEGATVWNGLEELVKESDRISA 360
QY 361 VANGKLNGVDCDEGETLVVGRPDGKGLGNASGAATVATLDRIRIAMSFLVMGLVSENP 420
DB 361 VANGKLNGVDCDEGETLVVGRPDGKGLGNASGAATVATLDRIRIAMSFLVMGLVSENP 420
QY 421 VTVDATMTATSFPPEFMDLMAGLGAKIELSDTKA 455
DB 421 VTVDATMTATSFPPEFMDLMAGLGAKIELSDTKA 455
RESULT 12
AAE39899
ID AAE39899 standard; protein; 455 AA.
XX
AC AAE39899;
XX
DT 18-DEC-2003 (first entry)
XX
DE Agrobacterium sp. strain CP4 class II EPSPS protein.
XX
KM Glyphosate tolerant 5-enolpyruvylshikimate-3-phosphate synthase; enzyme;
KM transgenic plant; transgenic; herbicide; weed control; EPSPS.
XX
OS Agrobacterium sp.
XX
PN US2002168680-A1.
XX
PD 14-NOV-2002.
XX
PF 16-DEC-1999; 99US-00464099.
XX
PR 31-AUG-1990; 90US-00576537.
PR 28-AUG-1991; 91US-00749611.
PR 13-SEP-1994; 94US-00306063.
PR 07-APR-1997; 97US-00833485.
PR 20-AUG-1998; 98US-00137440.
XX
PA (BARR/) BARRY G F.
PA (KISH/) KISHORE G M.
PA (PADG/) PADGETTE S R.
PA (STAL/) STALLINGS W C.
XX
PI Barry GF, Kishore GM, Padgette SR, Stallings WC;
XX
DR WPI; 2003-719984/68.
DR N-PSDB; AAD60590.
XX
PT New 5-enolpyruvylshikimate-3-phosphate synthase DNA sequence useful for
PT producing genetically transformed plants, and selectively controlling
PT weeds in a field containing crop having planted crop seeds or plants.
XX
PS Claim 5; Fig 3; 158pp; English.
XX
CC The invention relates to glyphosate tolerant 5-enolpyruvylshikimate-3-
CC phosphate synthase (EPSPS) enzymes and nucleic acid molecules encoding
CC such enzymes. The invention is useful for producing genetically
CC transformed plants which are tolerant to a glyphosate herbicide and for
CC selectively controlling weeds in a field containing a crop having planted
CC crop seeds or plants. The present sequence is Agrobacterium sp. strain
CC CP4 class II EPSPS protein
XX
SQ Sequence 455 AA;
Query Match 99.7%; Score 2282; DB 7; Length 455;

Best Local Similarity 99.8%; Pred. No. 3.6e-180;
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHGASRRATARKSSGSGTIRIPGDKSISRSFMFGGLASGETRITGLGGEVINTG 60
DB 1 MSHGASSPRATARKSSGSGTIRIPGDKSISRSFMFGGLASGETRITGLGGEVINTG 60
DB 61 KAMQAMGARIRKREGDWTIIDGVNGGLAPAPLDFGNATGCRITMGLVGYDPDSTFI 120
DB 61 KAMQAMGARIRKREGDWTIIDGVNGGLAPAPLDFGNATGCRITMGLVGYDPDSTFI 120
QY 121 GNASITKRPKMGVNLPLREMGVQVKSSEDGDRPLVTLRGKPTPTITTYRVPMASAOVKSAY 180
DB 121 GNASITKRPKMGVNLPLREMGVQVKSSEDGDRPLVTLRGKPTPTITTYRVPMASAOVKSAY 180
QY 181 LLAGANTPGITTVIEPIMTDRDTEKMLQGFGANLTVETDADGVRTIRLEGRKLTGOVID 240
DB 181 LLAGANTPGITTVIEPIMTDRDTEKMLQGFGANLTVETDADGVRTIRLEGRKLTGOVID 240
QY 241 VEGDPSSTAFPLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGSD 300
DB 241 VEGDPSSTAFPLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGSD 300
QY 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPILAVAAAFAGATVMNGLEELRYKESDRLSA 360
DB 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPILAVAAAFAGATVMNGLEELRYKESDRLSA 360
QY 361 VANGKLKNGVDCDEGTSLVVRGRPDGKLGNAAGAAVATHLDRHANSFLVMGLVSENP 420
DB 361 VANGKLKNGVDCDEGTSLVVRGRPDGKLGNAAGAAVATHLDRHANSFLVMGLVSENP 420
QY 421 VTVDATMTATSPPEFMDMAGLAKIELSDTKAA 455
DB 421 VTVDATMTATSPPEFMDMAGLAKIELSDTKAA 455

RESULT 13
AAR22301
ID AAR22301 standard; protein; 449 AA.
XX AAR22301;
AC AAR22301;
XX 24-OCT-2003 (revised)
DT 03-AUG-1992 (first entry)
XX
DE Class II BPSPS enzyme.
XX
KM Glyphosate tolerant bacteria; herbicides; glyphosate resistant plants;
KW 5'-enolpyruvylshikimate-3-phosphate synthase; weed control.
XX
OS Achromobacter sp; strain LBNA.
XX
PN WO9204449-A.
XX
PD 19-MAR-1992.
XX
PF 28-AUG-1991; 91WO-US006148.
XX
PR 31-AUG-1990; 90US-00576537.
XX
PA (MONS) MONSANTO CO.
XX
PI Barry GF, Kishore GM, Padgett SR;
XX
DR WPI; 1992-114356/14.
XX
XX DNA encoding class II 5'-enolpyruvyl shikimate-3-phosphate synthase - for
PT producing plants and bacteria tolerant to glyphosate herbicides.
XX
PS Disclosure; Fig 5; 148pp; English.
XX
CC The sequence is that of the Class II 5'-enolpyruvylshikimate-3 phosphate
CC synthase enzyme (BPSPS) of Achromobacter sp. strain LBNA It is used to

CC create glyphosate resistant plants or seeds which can be planted in a
CC field of crops to selectively control weeds. The crops selected for are
CC e.g. corn, wheat, rice, oilseed rape, tobacco and alfalfa. This provides
CC a cost effective, environmentally compatible weed control device. See
CC also AAR22300 and AAR22302. (Updated on 24-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 449 AA;
Query Match 83.1%; Score 1900.5; DB 2; Length 449;
Best Local Similarity 82.9%; Pred. No. 1.4e-148;
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

QY 1 MHGASRRATARKSSGSGTIRIPGDKSISRSFMFGGLASGETRITGLGGEVINTG 60
DB 1 MSHASPRATARKSSGSGTIRIPGDKSISRSFMFGGLASGETRITGLGGEVINTG 60
QY 61 KAMQAMGARIRKREGDWTIIDGVNGGLAPAPLDFGNATGCRITMGLVGYDPDSTFI 120
DB 61 KAMQAMGARIRKREGDWTIIDGVNGGLAPAPLDFGNATGCRITMGLVGYDPDSTFI 120
QY 121 GNASITKRPKMGVNLPLREMGVQVKSSEDGDRPLVTLRGKPTPTITTYRVPMASAOVKSAY 180
DB 121 GNASITKRPKMGVNLPLREMGVQVKSSEDGDRPLVTLRGKPTPTITTYRVPMASAOVKSAY 180
QY 181 LLAGANTPGITTVIEPIMTDRDTEKMLQGFGANLTVETDADGVRTIRLEGRKLTGOVID 240
DB 181 LLAGANTPGITTVIEPIMTDRDTEKMLQGFGANLTVETDADGVRTIRLEGRKLTGOVID 240
QY 241 VEGDPSSTAFPLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGSD 300
DB 241 VEGDPSSTAFPLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGSD 300
QY 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPILAVAAAFAGATVMNGLEELRYKESDRLSA 360
DB 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPILAVAAAFAGATVMNGLEELRYKESDRLSA 360
QY 361 VANGKLKNGVDCDEGTSLVVRGRPDGKLGNAAGAAVATHLDRHANSFLVMGLVSENP 420
DB 361 VANGKLKNGVDCDEGTSLVVRGRPDGKLGNAAGAAVATHLDRHANSFLVMGLVSENP 420
QY 421 VTVDATMTATSPPEFMDMAGLAKIELS 450
DB 418 VTVDSSNMATSPPEFMDMAGLAKIELS 447

RESULT 14
AAR22302
ID AAR22302 standard; protein; 449 AA.
XX AAR22302;
AC AAR22302;
XX 24-OCT-2003 (revised)
DT 03-AUG-1992 (first entry)
XX
DE Class II BPSPS enzyme.
XX
KM Glyphosate tolerant bacteria; herbicides; glyphosate resistant plants;
KW 5'-enolpyruvylshikimate-3-phosphate synthase; weed control.
XX
OS Pseudomonas sp; strain PG2982.
XX
PN WO9204449-A.
XX
PD 19-MAR-1992.
XX
PF 28-AUG-1991; 91WO-US006148.
XX
PR 31-AUG-1990; 90US-00576537.
XX
PA (MONS) MONSANTO CO.
XX
PI Barry GF, Kishore GM, Padgett SR;


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Db      121 GDASLSKRPMBGRVNLPLREMGVQVEADSDRMPLTLIGPKTANPLTYRVPMASAOVKSAY 180
Qy      181 LLAGINTPGITTVIEPIWTRDHTKMLQGFGANLTVETDADGVRTIRLEGKLTGQVID 240
Db      181 LLAGINTPGVTVIEPIWTRDHTKMLQGFGANLTVETDADGVRTIRLEGKLTGQVID 240
Qy      241 VGDPSSTAFPLVALLVPGSDVTLINVMNPTRTGLITLQEMGADIEVINPRLAGED 300
Db      241 VGDPSSTAFPLVALLVPGSDVTLINVMNPTRTGLITLQEMGADIEVINPRLAGED 300
Qy      301 VADLRVRSSTLKGVTVPEDRAPSMIDEYPIAFAAGATVMNGLEELRVKESDRLSA 360
Db      301 VADLRVRSSTLKGVTVPEDRAPSMIDEYPIAFAAGATVMNGLEELRVKESDRLSA 360
Qy      361 VANGKLKNGVDDEGETSLVVRGRPDGKLGNAAGAAVATHDRIAMGFLVMGLVSENP 420
Db      361 VANGKLKNGVDDEGETSLVVRGRPDGKLGNAAGAAVATHDRIAMGFLVMGLVSENP 420
Qy      421 VTDDATMTATSFPEFMDLMAIGAKIELS 450
Db      418 VTVDSDNMATISFPEFMDLMAIGAKIELS 447

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OM protein - protein search, using sw model

Run on: April 20, 2005, 15:19:11 ; Search time 73 Seconds
(without alignments)
3191.726 Million cell updates/sec

Title: US-10-622-201-70
Perfect score: 2288
Sequence: 1 MLHGASSRPATARKSSGLSG.....FMDLWAGLGAETLSDTKRA 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2288	100.0	455	2	Q71LY8 glycine max
2	2282	99.7	455	1	Q91464 agrobacteri
3	2088	91.7	455	1	ARO4_RTIME
4	1900.5	83.1	449	1	ARO4_PSES2
5	1881.5	82.2	450	1	ARO4_BRUSU
6	1874.5	81.9	450	1	ARO4_BRUMS
7	1855.5	81.1	450	1	ARO4_BRUAB
8	1783	77.9	452	1	ARO4_RRILLO
9	1505.5	65.8	442	2	Q6GKX3
10	1479.5	64.7	442	2	Q6GKX3
11	1252.5	54.7	445	2	Q6NDP4
12	1228.5	53.7	449	1	ARO4_BRAJA
13	1135	49.6	443	1	ARO4_CAUCR
14	989.5	43.2	746	2	Q9HZ69
15	970.5	42.4	746	2	Q88K05
16	942.5	41.2	748	2	Q6FA95
17	927.5	40.5	454	1	ARO4_XYLFY
18	916.5	40.1	438	1	ARO4_XANCP
19	912.5	39.9	440	1	ARO4_XYLFY
20	904.5	39.5	440	1	ARO4_XANAC
21	889	39.3	429	2	Q749Y6
22	884	38.6	431	1	ARAL_BACHD
23	879.5	38.4	429	1	ARO4_OCEIH
24	867.5	37.9	447	1	ARO4_SYNY3
25	850.5	37.2	440	1	ARO4_SYNEL
26	848	37.1	441	2	Q7U7H8
27	842.5	36.8	438	2	Q83E11
28	840.5	36.7	441	2	Q7V8F4
29	825	36.1	430	1	ARO4_STRP3
30	824.5	36.0	429	2	Q63A07
31	824.5	36.0	429	2	Q736A7

32	823.5	36.0	429	2	Q81C45	O81C45 bacillus ce
33	822	35.9	427	1	ARO4_STRP8	Q6Hf1 streptococ
34	820.5	35.9	429	1	Q6Hf8	Q6Hf8 bacillus th
35	820	35.8	430	1	ARO4_STRPY	Q9983 streptococ
36	817.5	35.7	423	1	ARO4_THENY	Q8r11 thermoaer
37	815.5	35.6	428	1	ARO4_LISTIN	Q9285 listeria in
38	813.5	35.6	427	1	ARO4_STRMU	Q8duv8 streptococ
39	813.5	35.6	427	1	ARO4_STRMU	Q8duv8 bacillus an
40	812	35.5	428	2	Q61P64	Q61P64 bacillus 11
41	807.5	35.3	432	2	Q7NLT3	Q7nlt3 gloebacter
42	806.5	35.2	430	1	ARO4_LACLA	Q9c90 lactococcus
43	806	35.2	443	1	ARO4_BACNO	Q4650 bacteroides
44	803.5	35.1	427	1	ARO4_STRPN	Q9e40 streptococ
45	802.5	35.1	430	1	ARO4_LACIC	P43905 lactococcus

ALIGNMENTS

RESULT 1	PRELIMINARY	PRT	455 AA.
Q71LY8			
Q71LY8			
AC	Q71LY8		
DT	05-JUL-2004 (TREMBLrel. 27, Created)		
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)		
DE	CP4RSPS.		
OS	Glycine max (soybean).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.		
OX	NCBI_TaxId=3847;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Son D.-Y., Lee S.-I.;		
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.		
CC	-1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =		
CC	phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.		
CC	-1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;		
CC	sixth step.		
CC	-1- SIMILARITY: Belongs to the EPSP synthase family.		
DR	EMBL; AF64188; AAL6757.1; -		
DR	GO; GO:0003866; P:3-phosphoshikimate 1-carboxyvinyltransferase. ; IEA.		
DR	GO; GO:0016740; P:transferase activity; IEA.		
DR	GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. . ; IEA.		
DR	InterPro; IPR006264; AroA_Ctransf.		
DR	InterPro; IPR001986; EPSP_synth.		
DR	Pfam; PF00275; EPSP synthase; 1.		
DR	Prodom; PD001867; EPSP synth; 1.		
DR	TIGRPFAM; TIGR01356; aroA; 1.		
DR	PROSITE; PS00104; EPSP_SYNTHASE_1; 1.		
DR	PROSITE; PS00885; EPSP_SYNTHASE_2; 1.		
KW	Amino-acid biosynthesis; Aromatic amino acid biosynthesis;		
KW	Transferase.		
SQ	SEQUENCE 455 AA; 47614 MW; C82D18307E4AD2C3 CRC64;		
Query Match	100.0%; Score 2288; DB 2; Length 455;		
Best Local Similarity	100.0%; Pred. No. 7.8e-129; Mismatches 0; Gaps 0;		
Matches	455; Conservative 0; Indels 0;		
QY	1	MLHGASSRPATARKSSGLSGTGRIPDDKISHSRPFMGGLASGETRITGLLBCEEDYINTG	60
DB	1	MLHGASSRPATARKSSGLSGTGRIPDDKISHSRPFMGGLASGETRITGLLBCEEDYINTG	60
QY	61	KAMQAMGARIRKEDGTWIIDGVNGGLAEPALDFGNATGCRITMGLVGVYDFDSTFI	120
DB	61	KAMQAMGARIRKEDGTWIIDGVNGGLAEPALDFGNATGCRITMGLVGVYDFDSTFI	120
QY	121	GPASLTFRMGVNLPLREMGVQVSEDDRLPYTLRGKTPPTTYRPMASAOVKSAY	180
DB	121	GPASLTFRMGVNLPLREMGVQVSEDDRLPYTLRGKTPPTTYRPMASAOVKSAY	180
QY	181	LLAGINTPGITTVIEIPIMTRDHTKMLQGFANLTVETDADGVRTIRLEGRKLTQOVID	240

Db	181	LLAGINTPGITTVIEPIIMTRDHTEKKLQGFSGANLVITETADGVRTIRLBESKGLTQGVID	240
Qy	241	VPGDSSSTAFPIVVAALLVPGSDVTLINVTMNPRTGLITLQMGADIEVINRRLAGGED	300
Db	241	VPGDSSSTAFPIVVAALLVPGSDVTLINVTMNPRTGLITLQMGADIEVINRRLAGGED	300
Qy	301	VADLRVSSTLKGVTVPEDRAPSMIDEPYLLAVAAAPFAGATVWNGLEELRVESDRLSA	360
Db	301	VADLRVSSTLKGVTVPEDRAPSMIDEPYLLAVAAAPFAGATVWNGLEELRVESDRLSA	360
Qy	361	VANGKLKLVGDDCEGETSLVVRGRPDGKGLGNAGSAAVAATHDRIAMSPFLWGLVSENP	420
Db	361	VANGKLKLVGDDCEGETSLVVRGRPDGKGLGNAGSAAVAATHDRIAMSPFLWGLVSENP	420
Qy	421	VTVDATMTATISFPFPMDLMAIGAKTIELSDTYAA	455
Db	421	VTVDATMTATISFPFPMDLMAIGAKTIELSDTYAA	455

RESULT 2

ID	_ARO	AGRSP	STANDARD;	PRT;	455 AA.
AC		QPR4E4;			
DT	30-MAY-2000	(Rel. 39, Created)			
DT	30-MAY-2000	(Rel. 39, Last sequence update)			
DT	05-JUN-2004	(Rel. 44, Last annotation update)			
DE	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)	(5-enoilpruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).			
GN	Name=aroA;				
OS	Agrobacterium sp. (strain CP4).				
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;				
OC	Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.				
OX	NCBI_TaxId=361;				
RN	[1]				
RP	SEQUENCE FROM N.A. AND SEQUENCE OF 1-28; 47-61 AND 321-333.				
RA	Barry G.F., Kishore G.M., Padgett S.R., Stallings W.C.;				
RT	"Glutamate-tolerant 5-enoilpruvylshikimate-3-phosphate synthases."				
RL	Patent number US5633435, 27-MAY-1997.				
RN	[2]				
RP	SEQUENCE OF 1-15.				
RX	MEDLINE=96182485; PubMed=8598558;				
RA	Harrison L.A., Bailey M.R., Naylor M.W., Ream J.E., Hammond B.G.,				
RA	Mida D.L., Burnette B.L., Nickson T.E., Miteky T.A., Taylor M.L.,				
RA	Fuchs R.L., Padgett S.R.;				
RT	"The expressed protein in glutamate-tolerant soybean, 5-enoilpruvylshikimate-3-phosphate synthase from Agrobacterium sp.				
RT	strain CP4, is rapidly digested in vitro and is not toxic to acutely				
RT	gavaged mice."				
RL	J. Nutr. 126:728-740(1996).				
CC	-1. CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.				
CC	-1. PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway; sixth step.				
CC	-1. SUBCELLULAR LOCATION: Cytoplasmic (Probable).				
CC	-1. BIOTECHNOLOGY: Introduced by genetic manipulation and expressed in glutamate-tolerant soybean, canola, cotton and maize by Monsanto.				
CC	Developed to provide new weed-control options for farmers.				
CC	Expression of this protein in plants imparts high levels of glutamate tolerance.				
CC	-1. SIMILARITY: Belongs to the EPSP synthase family.				
DR	HAMAP; MF_00210; -; 1.				
DR	InterPro; IPR006264; AroA.				
DR	InterPro; IPR001986; EPSP_synth.				
DR	Pfam; PF000275; EPSP_synthase; 1.				
DR	ProDom; PD001867; EPSP_synth; 1.				
DR	TIGRFAMs; TIGR01356; aroA; 1.				
DR	PROSITE; PS00104; EPSP_SYNTHASE_1; 1.				
DR	PROSITE; PS00885; EPSP_SYNTHASE_2; 1.				
KW	Aromatic amino acid biosynthesis; Direct protein sequencing;				
FT	Genetically modified food, Herbicide resistance; Transferase.				
FT	CONFLICT 2 2				
FT	SEQUENCE 455 AA; 4758 MW; 23658000806EFA22 CRC64;				
FT	SEQUENCE 455 AA; 4758 MW; 23658000806EFA22 CRC64;				

Query Match	99.7%	Score 2282;	DB 1;	Length 455;
Best Local Similarity	99.8%;	Pred. No. 1.8e-128;		
Matches 454; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1	MLHGASSPAPATARKSSGLSGTVRI	IPGDYS	ISHRSMFPGGLASGETRITGLLEGEDYINNG	60
Db	1	MSHGASSPAPATARKSSGLSGTVRI	IPGDKSI	SHRSMFPGGLASGETRITGLLEGEDYINNG	60
QY	61	KAMQAMGARIRIEEGDTWIIIDGVNGGLLAPEAPLDFGNATSCRLTMGLVGYVDFPSTFI			120
Db	61	KAMQAMGARIRIEEGDTWIIIDGVNGGLLAPEAPLDFGNATSCRLTMGLVGYVDFPSTFI			120
QY	121	GDA\$ITKKA PMGRVNIPLREMGVQVKS EEDGBRLPVTIRGKTEPTIITYRVPMASAOYK\$AV			180
Db	121	GDA\$ITKKA PMGRVNIPLREMGVQVKS EEDGBRLPVTIRGKTEPTIITYRVPMASAOYK\$AV			180
QY	181	LLAGINTP\$GITTIVIEPIINTRODTEKMLQFGFANLVEITDADQVTRITLEGCKLTQ\$OVID			240
Db	181	LLAGINTP\$GITTIVIEPIINTRODTEKMLQFGFANLVEITDADQVTRITLEGCKLTQ\$OVID			240
QY	241	VPGP\$P\$STAFPLV\$ALLVPGSDVITL\$NLMNPTRTGLILTLQ\$EMGADIEVINPRL\$AGSD			300
Db	241	VPGP\$P\$STAFPLV\$ALLVPGSDVITL\$NLMNPTRTGLILTLQ\$EMGADIEVINPRL\$AGSD			300
QY	301	VADLRVRSSTLKGTVVPE\$DRA\$PSMIDEXPIILAVAA\$P\$EAGAVNMNGLIELR\$KES\$RLSA			360
Db	301	VADLRVRSSTLKGTVVPE\$DRA\$PSMIDEXPIILAVAA\$P\$EAGAVNMNGLIELR\$KES\$RLSA			360
QY	361	VANGIKLNGVDCDEGE\$TSLVVRGRPDGKGLGNA\$GAAVATHLIDHRIAMSFLVMGLV\$SENP			420
Db	361	VANGIKLNGVDCDEGE\$TSLVVRGRPDGKGLGNA\$GAAVATHLIDHRIAMSFLVMGLV\$SENP			420
QY	421	VTVDDATMIATISFPE\$FMDL\$MAGL\$AKIEL\$STDKAA	455		
Db	421	VTVDDATMIATISFPE\$FMDL\$MAGL\$AKIEL\$STDKAA	455		

RESULT 3

ID	AROA_RHIME	STANDARD;	PRT;	455 AA.
AC	0925V5			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-			
DE	enolpyruvylshikimate-3-phosphate synthase) (BSP synthase) (BSPS).			
CN	Name=aroA, OrderedLocusNames=R00253, ORFNames=Smc00333,			
OS	Rhizobium meliloti (Sinorhizobium meliloti).			
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;			
OC	Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.			
OX	NCBI_TaxID=382;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=1021.			
FX	MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;			
RA	Capela D., Barloy-Hublier F., Gouzy O., Boche G., Ampe F., Batut J.,			
RA	Bostard P., Becker A., Boutry M., Cadieu E., Driano S., Gloux S.,			
RA	Godie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Maury D.,			
RA	Pohl T., Portetelle D., Puelher A., Punelle B., Ramseger U.,			
RA	Renard C., Trebault P., Vandenbol M., Waidner S., Galibert F.;			
RT	"Analysis of the chromosome sequence of the legume symbiont			
RT	Sinorhizobium meliloti strain 1021."			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).			
CC	-1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =			
CC	phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.			
CC	-1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;			
CC	sixth step.			
CC	-1- SUBUNIT: Monomer (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).			
CC	-1- SIMILARITY: Belongs to the BSPS synthase family.			
CC	-----			
CC	This SWISS-PROT entry is copyright it is produced through a collaboration			

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DR EMBL: AL591783; CAC41690.1; --
 DR HAMAP: MF_00210; -- 1.
 DR InterPro: IPR006264; AroA.
 DR InterPro: IPR001986; EPSP_synth.
 DR Pfam: PF00275; EPSP_synthase; 1.
 DR ProDom: PD001867; EPSP_synth; 1.
 DR TIGRFAMs: TIGR01356; aroA; 1.
 DR PROSITE: PS00104; EPSP_SYNTHASE_1; 1.
 DR PROSITE: PS00885; EPSP_SYNTHASE_2; 1.
 DR Aromatic amino acid biosynthesis; Complete proteome; Transferase.
 KM SEQUENCE 455 AA; 47900 MW; 97659E1C7B1021B5 CRC64;

Query Match 91.7%; Score 2098; DB 1; Length 455;
 Best Local Similarity 90.5%; Pred. No. 1.8e-117;
 Matches 412; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

QY 1 MLHGSRPATARKSGSGTIVRIPGDKSISRSFMFGGLASGETRITGLGEGDVINTG 60
 DB 1 MSHGSNPRATARKSDDLKGTIRIPDKSISRSFMFGGLAAGETRITGLGEGDVINTG 60
 QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPEAPLDFGNAATGCRITLMTGLVGYDPTSTI 120
 DB 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPEAPLDFGNAATGCRITLMTGLVGYDPTSTI 120
 QY 121 GNASLTKRPMGVNPLRMEGVQVKSSEDRLPVTLRGKPTPTPIYRVPMASQVKSXAV 180
 DB 121 GNASLTKRPMGVNPLRMEGVQVKSSEDRLPVTLRGKPTPTPIYRVPMASQVKSXAV 180
 QY 181 LLAGANTPGITTVIEPIMRDHTKMLQGFGANLTVETDADGVRTIRLEGRGLTGQVID 240
 DB 181 LLAGANTPGITTVIEPIMRDHTKMLQGFGANLTVETDADGVRTIRLEGRGLTGQVID 240
 QY 241 VEGDPSSTAFPLVALLVPGSDVTILNVLMNPTRTGLITLQEMGADIVINPRLAGSD 300
 DB 241 VEGDPSSTAFPLVALLVPGSDVTILNVLMNPTRTGLITLQEMGADIVINPRLAGSD 300
 QY 301 VADLVRSTLKGTVPEDRAPSMIDEVPIVLAFAAGATVMNGLEELRYKESDRLSA 360
 DB 301 VADLVRSTLKGTVPEDRAPSMIDEVPIVLAFAAGATVMNGLEELRYKESDRLSA 360
 QY 361 VANGKLKNGVDCDEGTSLVVGRPDGKLGNAAGAAVATHLDRITAMSFVWGLVSENP 420
 DB 361 VANGKLKNGVDCDEGTSLVVGRPDGKLGNAAGAAVATHLDRITAMSFVWGLVSENP 420
 QY 421 VTVDATMIATSPPEFMDIAGAKIELSDTYKA 455
 DB 421 VTVDATMIATSPPEFMDIAGAKIELSDTYKA 455

RESULT 4
 AROA_PSES2 STANDARD; PRT; 449 AA.

ID AROA_PSES2 STANDARD; PRT; 449 AA.
 AC P56952;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
 GN enoIpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPs).
 OS Pseudomonas sp. (strain PG2982), and
 OS Acetobacter sp. (strain LBAA).
 OC Bacteria; Proteobacteria.
 OC NCBI_TaxID=308, 129026;
 RN (1)
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 2-16.
 RP Barry G.F., Kishore G.M., Padgett S.R., Stallings W.C.;

RT "Glyphosate-tolerant 5-enoIpyruvylshikimate-3-phosphate synthases."
 RL Patent number US633435, 27-MAY-1997.
 CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
 CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 CC sixth step.

CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- MISCELLANEOUS: Resistant to the antibiotic glyphosate.
 CC -1- SIMILARITY: Belongs to the EPSP synthase family.
 DR HAMAP: MF_00210; -- 1.
 DR InterPro: IPR006264; AroA.
 DR InterPro: IPR001986; EPSP_synth.
 DR Pfam: PF00275; EPSP_synthase; 1.
 DR ProDom: PD001867; EPSP_synth; 1.
 DR TIGRFAMs: TIGR01356; aroA; 1.
 DR PROSITE: PS00104; EPSP_SYNTHASE_1; 1.
 DR PROSITE: PS00885; EPSP_SYNTHASE_2; 1.
 DR Aromatic amino acid biosynthesis; Direct protein sequencing;
 KW Herdicide resistance; Transferase.
 KM SEQUENCE 449 AA; 47297 MW; 447F213EECCAEFC1 CRC64;

Query Match 83.1%; Score 1900.5; DB 1; Length 449;
 Best Local Similarity 82.9%; Pred. No. 1.1e-105;
 Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

QY 1 MLHGSRPATARKSGSGTIVRIPGDKSISRSFMFGGLASGETRITGLGEGDVINTG 60
 DB 1 MSHGSNPRATARKSDDLKGTIRIPDKSISRSFMFGGLAAGETRITGLGEGDVINTG 60
 QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPEAPLDFGNAATGCRITLMTGLVGYDPTSTI 120
 DB 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPEAPLDFGNAATGCRITLMTGLVGYDPTSTI 120
 QY 121 GNASLTKRPMGVNPLRMEGVQVKSSEDRLPVTLRGKPTPTPIYRVPMASQVKSXAV 180
 DB 121 GNASLTKRPMGVNPLRMEGVQVKSSEDRLPVTLRGKPTPTPIYRVPMASQVKSXAV 180
 QY 181 LLAGANTPGITTVIEPIMRDHTKMLQGFGANLTVETDADGVRTIRLEGRGLTGQVID 240
 DB 181 LLAGANTPGITTVIEPIMRDHTKMLQGFGANLTVETDADGVRTIRLEGRGLTGQVID 240
 QY 241 VEGDPSSTAFPLVALLVPGSDVTILNVLMNPTRTGLITLQEMGADIVINPRLAGSD 300
 DB 241 VEGDPSSTAFPLVALLVPGSDVTILNVLMNPTRTGLITLQEMGADIVINPRLAGSD 300
 QY 301 VADLVRSTLKGTVPEDRAPSMIDEVPIVLAFAAGATVMNGLEELRYKESDRLSA 360
 DB 301 VADLVRSTLKGTVPEDRAPSMIDEVPIVLAFAAGATVMNGLEELRYKESDRLSA 360
 QY 361 VANGKLKNGVDCDEGTSLVVGRPDGKLGNAAGAAVATHLDRITAMSFVWGLVSENP 420
 DB 361 VANGKLKNGVDCDEGTSLVVGRPDGKLGNAAGAAVATHLDRITAMSFVWGLVSENP 420
 QY 421 VTVDATMIATSPPEFMDIAGAKIELSDTYKA 450
 DB 421 VTVDATMIATSPPEFMDIAGAKIELSDTYKA 450

RESULT 5
 AROA_BRUSU STANDARD; PRT; 450 AA.

ID AROA_BRUSU STANDARD; PRT; 450 AA.
 AC O8G3C4;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
 GN enoIpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPs).
 OS Name=aroA; Ordered locus Names=BR0025;
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OC NCBI_TaxID=29461;


```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biotype 1;
RX MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin A.S., Koloney J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A.,
RA Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
RA Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
RA Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13146-13153 (2002).
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC sixth step.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AB014317; AAN28982.1; -.
DR TIGR; BR0025; -.
DR HAMAP; MF_00210; -. 1.
DR InterPro; IPR006264; AroA.
DR InterPro; IPR001986; EPSP synth.
DR Pfam; PF00275; EPSP synthase; 1.
DR Prodom; PDO01867; EPSP_synth; 1.
DR TIGRFAMs; TIGR01356; aroA; 1.
DR PROSITE; PS00104; EPSP SYNTHASE 1; 1.
DR PROSITE; PS00885; EPSP SYNTHASE 2; 1.
DR Aromatic amino acid biosynthesis; Complete proteome; Transferase.
SQ SEQUENCE 450 AA; 47249 MW; E571FAB83C049PDC CRC64;

Query Match 82.2%; Score 1861.5; DB 1; Length 450;
Best Local Similarity 82.6%; Pred. No. 1.5e-104;
Matches 369; Conservative 33; Mismatches 42; Indels 3; Gaps 1;

OY 1 MHGSSRPATARKSGSGTIRIPGDKSISHRSFMFGGLASGERTITGLLEGEDVINTG 60
DB 1 MSHSACPATARKHSQLTGEIRIPEDKSIHSRSMFGLASGKTRITGLLEGEDVINTG 60
OY 61 KAMQMGARIRKEGDTWIIDVGNGLLAPAPLDFGNATGCRITMGLVGVYDPDSPTI 120
DB 61 RAMQMGARIRKEGDTWIIDVGNGLLAPAPLDFGNATGCRITMGLVGVYDPDSPTI 120
OY 121 GPASLTFRPMGVNLPFRMGVQVKSSEDGRLPVLRGKPTPIPTIRYVMAAQVKSAY 180
DB 121 GPASLTFRPMGVNLPFRMGVQVKSSEDGRLPVLRGKPTPIPTIRYVMAAQVKSAY 180
OY 121 GPASLTFRPMGVNLPFRMGVQVKSSEDGRLPVLRGKPTPIPTIRYVMAAQVKSAY 180
DB 121 GPASLTFRPMGVNLPFRMGVQVKSSEDGRLPVLRGKPTPIPTIRYVMAAQVKSAY 180
OY 181 LLAGINTPGITVIRIMRDTHEKMLQSGFANLIVETDADGRTTRLEGRCRLTQGVVD 240
DB 181 LLAGINTPGITVIRIMRDTHEKMLQSGFANLIVETDADGRTTRLEGRCRLTQGVVD 240
OY 241 VPGDSSSTAFPLVAALLVPGSDVTILNVAMNPTRTGLITLQEMGADIVINPRLAGSD 300
DB 241 VPGDSSSTAFPLVAALLVPGSDVTILNVAMNPTRTGLITLQEMGADIVINPRLAGSD 300
OY 301 VADLRVRSSTLKVTVYEDRPASMIIDYPLILAVAAAFAGATVWNGLEELRYKESDRLSA 360
DB 301 VADLRVRSSTLKVTVYEDRPASMIIDYPLILAVAAAFAGATVWNGLEELRYKESDRLSA 360
OY 361 VANGIKLNVDDDEGTSILVGRPRGKGLGNAAGAAVATHLDHRLAMSFVWGLVSENP 420
DB 361 VANGIKLNVDDDEGTSILVGRPRGKGLGNAAGAAVATHLDHRLAMSFVWGLVSENP 420

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DB 361 VARGLEANGVDCTESENMLTYRGPRGKGLG---GGTATVTHLDRIRANSFLVWGLASEKP 417
OY 421 VTVDATVATSPFPEFMDLMAGLAKI 447
DB 418 VTVDSTVATSPFPEFMDLMAGLAKI 444

RESULT 6
AEOA BRUME STANDARD; PRT; 450 AA.
ID AEOA BRUME
AC 08YEG1;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update) (SC 2.5.1.19) (5-
DE 3-phosphoshikimate 1-carboxyvinyltransferase (EPSP synthase) (EPSPS) .
GN Name=aroA; Ordered locus names=BME11917;
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxId=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX PubMed=11756688; DOI=10.1073/pnas.221575398;
RA Delvecchio V.G., Kapetral V., Redkar R.U., Patra G., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonki L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyriides N.C., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC sixth step.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AB009625; AAL53098.1; ALT_INIT.
DR HAMAP; MF_00210; -. 1.
DR InterPro; IPR006264; AroA.
DR InterPro; IPR001986; EPSP synth.
DR Pfam; PF00275; EPSP synthase; 1.
DR Prodom; PDO01867; EPSP_synth; 1.
DR TIGRFAMs; TIGR01356; aroA; 1.
DR PROSITE; PS00104; EPSP SYNTHASE 1; 1.
DR PROSITE; PS00885; EPSP SYNTHASE 2; 1.
DR Aromatic amino acid biosynthesis; Complete proteome; Transferase.
SQ SEQUENCE 450 AA; 47207 MW; 931C4B83C162CB7 CRC64;

Query Match 81.9%; Score 1874.5; DB 1; Length 450;
Best Local Similarity 82.1%; Pred. No. 4e-104;
Matches 367; Conservative 34; Mismatches 43; Indels 3; Gaps 1;

OY 1 MHGSSRPATARKSGSGTIRIPGDKSISHRSFMFGGLASGERTITGLLEGEDVINTG 60
DB 1 MSHSACPATARKHSQLTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTG 60
OY 61 KAMQMGARIRKEGDTWIIDVGNGLLAPAPLDFGNATGCRITMGLVGVYDPDSPTI 120
DB 61 RAMQMGARIRKEGDTWIIDVGNGLLAPAPLDFGNATGCRITMGLVGVYDPDSPTI 120

```

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QY 121 GDA$LTRKRMGRVNLRLRMGVQVKSDEDDRLPVLTRGKPTPTTYRYVPMASQVKSAY 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GDA$ISKRMGRVNLRLRMGVQVKAEBGRMPLTLIGRTANPIAYRVPMASQVKSAY 180
QY 181 LLAGNTPGITTVIEPIWTRDHEKMLQGPGANLTYETDADGVRTIRLGRGKLTQOVID 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LLAGNTPGITTVIEPIWTRDHEKMLQGPGADLTVEYTDKDGVRHIRIVGQGLTQOTID 240
QY 241 VEGDE$STAFPLVAALLVPGSDVTILNVLMNPTRTGLITLQEMGADIEVINPRLAGSD 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 VEGD$BSTAFPLVALLVGE$DVTILNVLMNPTRTGLITLQEMGADIEIDPRLAGSD 300
QY 301 VADLRV$STLKGVTVPEDRAPSMIDEPYLLAAVAAFAEGATVWNGLEELRVKESDRLSA 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 VADLRV$KSKLKGVTVPEDRAPSMIDEPYLLAAVAAFAEGATVWNGLEELRVKESDRLSA 360
QY 361 VANGKLTNGVDCDEG$TSLVGRPGDKLGNASGAAVATHLDHRIAM$FLVWGLVSENP 420
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 VARGLEANGVDCDEG$MSLTVRGRPGDKLG--GGTVATHLDHRIAM$FLVWGLVSENP 417
QY 421 VTVDDATMTATSPPEFMDLMA$GLAKI 447
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 418 VTVDD$TMTATSPPEFMDLMA$GLAKI 444

```

RESULT 7

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ARO$ BRUAB
ID ARO$ BRUAB STANDARD; PRT; 450 AA.
AC 09AGV2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
  enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).
GN Name=aroA;
OS Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bacteriella; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OX NCBI_TaxId=235;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2308;
RA Gan T., Essenberg R.C.;
RT "Characterization of the aroA gene of Brucella abortus and
  construction of an aroA mutant.";
RU Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
  phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
  six step.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
-----
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  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@sib-sib.ch).
-----
CC EMBL: AF26475; AKK27445.1; ALT_INT.
CC HAMAP: MF_000210; -1.
CC InterPro: IPR006264; AroA.
CC InterPro: IPR001986; EPSP synth.
CC Pfam: PF00275; EPSP synthase; 1.
CC ProDom: PD001867; EPSP synth; 1.
CC TIGRFAMs: TIGR01356; aroA; 1.
CC PROSITE: PS00104; EPSP SYNTHASE_1; 1.
CC PROSITE: PS00885; EPSP SYNTHASE_2; 1.
CC Aromatic amino acid biosynthesis; Transferase.
KW SEQUENCE 450 AA; 47264 MW; 371B9F97B2ED9DA4 CRC64;
SQ

```

Query Match 81.1%; Score 1855.5; DB 1; Length 450;
 Best Local Similarity 81.4%; Pred. No. 5,5e-103;
 Matches 364; Conservative 35; Mismatches 45; Indels 3; Gaps 1;

```

QY 1 MHHGASSRPAATARKSSGLSGTVRIIPGDKSISHR$FMFGGLASGETITGLB$EDVIYNG 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MSH$ACPKPRATARH$QALTG$IRIPGDKSISHR$FMFGGLASGETITGLB$EDVIYNG 60
QY 61 KAMQAMGARIRKRGDPMIIDGVNGGLAP$APLIDG$NATGCRITMGLVGVDPDSTFI 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 KAMQAMGARIRKRGDPMIIDGVNGGLAP$APLIDG$NATGCRITMGLVGVDPDSTFI 120
QY 121 GDA$LTRKRMGRVNLRLRMGVQVKSDEDDRLPVLTRGKPTPTTYRYVPMASQVKSAY 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GDA$ISKRMGRVNLRLRMGVQVKAEBGRMPLTLIGRTANPIAYRVPMASQVKSAY 180
QY 181 LLAGNTPGITTVIEPIWTRDHEKMLQGPGANLTYETDADGVRTIRLGRGKLTQOVID 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LLAGNTPGITTVIEPIWTRDHEKMLQGPGADLTVEYTDKDGVRHIRIVGQGLTQOTID 240
QY 241 VEGDE$STAFPLVAALLVPGSDVTILNVLMNPTRTGLITLQEMGADIEVINPRLAGSD 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 VEGD$BSTAFPLVALLVGE$DVTILNVLMNPTRTGLITLQEMGADIEIDPRLAGSD 300
QY 301 VADLRV$STLKGVTVPEDRAPSMIDEPYLLAAVAAFAEGATVWNGLEELRVKESDRLSA 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 VADLRV$KSKLKGVTVPEDRAPSMIDEPYLLAAVAAFAEGATVWNGLEELRVKESDRLSA 360
QY 361 VANGKLTNGVDCDEG$TSLVGRPGDKLGNASGAAVATHLDHRIAM$FLVWGLVSENP 420
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 VARGLEANGVDCDEG$MSLTVRGRPGDKLG--GGTVATHLDHRIAM$FLVWGLVSENP 417
QY 421 VTVDDATMTATSPPEFMDLMA$GLAKI 447
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 418 VTVDD$TMTATSPPEFMDLMA$GLAKI 444

```

RESULT 8

```

ARO$ RHIL0
ID ARO$ RHIL0 STANDARD; PRT; 452 AA.
AC 098CC1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
  enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).
GN Name=aroA; Ordered locus Names=ml15213;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OX NCBI_TaxId=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFE30309;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
  Watanabe A., Ideesawa K., Ishikawa A., Kawashima K., Kimura T.,
  Kishida Y., Kiyokawa C., Kohara M., Matsuno M., Matsuno A.,
  Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
  Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
  Mesorhizobium loti.";
RL DNA Res. 7:331-338 (2000).
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
  phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
  six step.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
-----
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 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL, AP003006; BAB51700.1; --
 DR HAMAP; MF_00210; -, 1.
 DR InterPro; IPR006264; ArcoA.
 DR InterPro; IPR001986; Epsp synth.
 DR Pfam; PF00275; Epsp synthase; 1.
 DR Prodom; PPO01867; Epsp synth; 1.
 DR TIGRfam; TIGR01356; arcoA; 1.
 DR PROSITE; PS00104; Epsp SYNTHASE 1; 1.
 DR PROSITE; PS00885; Epsp SYNTHASE 2; 1.
 DR Aromatic amino acid biosynthesis; Complete proteome; Transferase.
 KW SEQUENCE 452 AA; 47455 MW; 2B593E3523B938 CRC64;
 SQ

Query Match 77.9%; Score 1783; DB 1; Length 452;
 Best Local Similarity 77.8%; Pred. No. 1.2e-98;
 Matches 351; Conservative 33; Mismatches 63; Indels 4; Gaps 2;

QY 1 MHGASRPATARKSGLSGTWIRIPGDKSISHSFWMFGGLASGETRITGLLEGEDVINTG 60
 DB 1 MSHAAAPATARKSOALSSTNARVPEDKSISHSFWMFGGLASGETRITGLLEGEDVMTG 60

QY 61 KAMQAMGARIRKEDTWIIDVNGGGLAPEAPLDFGNATGCRITMGLVGVDPSTFPI 120
 DB 61 AAMKAMGAHIEKGAEMWIRGTGNGLIQPEGLDFGNAGTSRLTMGLVGVDMETPI 120

QY 121 GPASITKPMGVNLPRLRMGVQV-KSEIDGRLEVTLRGPKPTPTTYRPMASQVSKA 179
 DB 121 GPASISGPMGVNLEPLRMGVQVLEKATPGDMPTILHGPKAAPTYRPMASQVSKA 180

QY 121 GPASISGPMGVNLEPLRMGVQVLEKATPGDMPTILHGPKAAPTYRPMASQVSKA 180
 DB 121 GPASISGPMGVNLEPLRMGVQVLEKATPGDMPTILHGPKAAPTYRPMASQVSKA 180

QY 180 VLLAGLMPGITTVIEPIITRDHTEKMLQGFANLTVETDADGVRTIRLEGKGLTGVYI 239
 DB 181 VLLAGLMPGITTVIEPIITRDHTEKMLQGFANLTVETDADGVRTIRLEGKGLTGVYI 240

QY 240 DVPGPSSTAPFLVALALVPGSDVTILNVLNMPTRTGLITLQMGADIEVINPLRAGE 299
 DB 241 AVGPSSAGPFLVALALVPGSDITENVLNMPTRTGLITLQMGQGLDIINPRAGE 300

QY 300 DYADIRVSSITKGVTVPEDRAPSMIDEPYPIAVALAFAEGATWNGLEELRYKESDRIS 359
 DB 301 DYADIRVRSSELKGAVALPERAPSMIDEPYPIAVALAFAEGATWNGLEELRYKESDRIS 360

QY 360 AVANGKLINGVDCDEGETSLVVRGPRDGKIG--NAGAAVATHLDRHIAHSFLVMGLV 416
 DB 361 AVANGKLINGVDCDEGETSLVVRGPRDGKIG--NAGAAVATHLDRHIAHSFLVMGLV 420

QY 417 SENPVTDATMTATSPFEMDLMAIGAKI 447
 DB 421 TEKPVTTIDQAMTATSFPFEMDLMAIGAKI 451

RESULT 9
 O6G0X3 PRELIMINARY; PRT; 442 AA.
 AC O6G0X3;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE 3-phosphoshikimate 1-carboxyvinyltransferase.
 GN Name=arcoA; OrderedlocusNames=B000880;
 OS Bartonella quintana (Rochalimaea quintana).
 OC Bacteriia; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bartonellaceae; Bartonella.
 NC NCB1_TaxID=803;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=nonlouse;
 RX PubMed=15210978; DOI=10.1073/pnas.0305659101;

RA Almark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,
 RA Candaeck B., Eriksson A.-S., Naesslund A.K., Handley S.A., Huvel M.,
 RA La Scola B., Holmberg M., Andersson S.G.E.;
 RT "The louse-borne human pathogen Bartonella quintana is a genomic
 RT derivative of the zoonotic agent Bartonella henselae.",
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
 CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
 CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 CC sixth step.
 CC -1- SIMILARITY: Belongs to the Epsp synthase family.
 DR EMBL; BX897700; CAP25595.1; --
 DR GO; GO:0003866; F-3-phosphoshikimate 1-carboxyvinyltransferase. . .; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. . .; IEA.
 DR InterPro; IPR006264; ArcoA Transf.
 DR InterPro; IPR001986; Epsp synth.
 DR Pfam; PF00275; Epsp synthase; 1.
 DR Prodom; PPO01867; Epsp synth; 1.
 DR TIGRfam; TIGR01356; arcoA; 1.
 DR PROSITE; PS00104; Epsp SYNTHASE 1; 1.
 KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
 KW Complete proteome; Transferase.
 SQ SEQUENCE 442 AA; 47538 MW; 225F15BCDF6DBBA CRC64;

Query Match 65.8%; Score 1505.5; DB 2; Length 442;
 Best Local Similarity 68.1%; Pred. No. 4.5e-82;
 Matches 299; Conservative 51; Mismatches 86; Indels 3; Gaps 1;

QY 9 PATARKSGLSGTWIRIPGDKSISHSFWMFGGLASGETRITGLLEGEDVINTGKAMQAMGA 68
 DB 6 PTTAKSKTCLSGKITIPDKSISHSRLTLGGIANETHHGLGDDVLANTAQAQAMGA 65

QY 69 RIRKEDTWIIDVNGGGLAPEAPLDFGNATGCRITMGLVGVDPSTFPGASLTKR 128
 DB 66 CIKKADMIIRGTNGGLAKERKPLNFGMGTGARLVMGVNAPYHMKTTFFIGASLSR 125

QY 129 PMGVNLPRLRMGVQVKEEDGRLEPYLRGPKPTPTTYRPMASQVSKAVLGLNTP 188
 DB 126 PMGRILNPLRLMGVIEATHTGRPLPLTYGPMANPIRYRIPASQVSKATILGLNTP 185

QY 189 GITYTIEPIITRDHTEKMLQGFANLTVETDADGVRTIRLEGKGLTGVYIDVDPGST 248
 DB 186 GTTYTIEPIITRDHTEKMLQGFANLTVETDADGVRTIRLEGKGLTGVYIDVDPGST 245

QY 249 AFLVALALVPGSDVTILNVLNMPTRTGLITLQMGADIEVINRLAGGEDVADLRYS 308
 DB 246 AFLPIIALLVNSDITENVLNLSRMGLIETLMDAKITELNQHKTGGENVADLRYS 305

QY 309 STLKGVTVPEDRAPSMIDEPYPIAVALAFAEGATWNGLEELRYKESDRISAVANGKLIN 368
 DB 306 SMLKGVTVPEKERAPSMIDEPYPIAVALAFAEGATWNGLEELRYKESDRISLAAGKLIN 365

QY 369 GVDCEGETSLVVRGPRDGKIGNAGAAVATHLDRHIAHSFLVMGLVSENPVTDATM 428
 DB 366 HVDCEEKDFLIVHGXSAKIG--GGVTTTHLDRHIAHSFLVGLVSEKPVTTIDKRM 422

QY 429 IATSFPEFMDLMAIGAKI 447
 DB 423 IATSFPEFPIFQGLGKI 441

RESULT 10
 O6G545 PRELIMINARY; PRT; 442 AA.
 AC O6G545;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE 3-phosphoshikimate 1-carboxyvinyltransferase.
 GN Name=arcoA; OrderedlocusNames=BH00950;
 OS Bartonella henselae (Rochalimaea henselae).
 OC Bacteriia; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Bartonellaceae; Bartonella.
 OX NCBI_Taxid=38323;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 49882 / Houston 1;
 RX PubMed=15210978; DOI=10.1073/pnas.0305659101;
 RA Almark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,
 RA Camdeack B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvel M.,
 RA La Scola B., Holmberg M., Andersson S.G.E.;
 RT "The louse-borne human pathogen Bartonella quintana is a genomic
 RT derivative of the zoonotic agent Bartonella henselae";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721 (2004)
 CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
 CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 CC sixth step.
 CC -1- SIMILARITY: Belongs to the EPSP synthase family.
 DR EMBL; BX897699; CAF26911.1; -
 DR GO; GO:0003866; F:3-phosphoshikimate 1-carboxyvinyltransferase. . .; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. . .; IEA.
 DR InterPro; IPR006264; AroA Ctransf.
 DR InterPro; IPR001986; EPSP_synth.
 DR Pfam; PF00275; EPSP_synthase; 1.
 DR ProDom; PD001867; EPSP_synthase; 1.
 DR TIGRFAMs; TIGR01356; aroA; 1.
 DR PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
 KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
 KW Complete proteome; Transferase.
 SQ SEQUENCE 442 AA; 47515 MW; 1B9D1F951BE1982D CRC64;

Query Match 64.7%; Score 1479.5; DB 2; Length 442;
 Best Local Similarity 67.0%; Pred. No. 1.6e-80;
 Matches 294; Conservative 52; Mismatches 90; Indels 3; Gaps 1;

OY 9 PATARKSSGLSGTVIRPGDKSISHRSFMFGGLASGETRTITGLLEGEDVINTGKAMQAMGA 68
 DB 6 PMTAVKSTRLSGIKIPGDKSISHRSLIIGGLASGETHTHIGLIESDVENTAAMQALGA 65
 OY 69 RIRKEDGTTIIDGVNGGLAPAPLDPGNAATGCLTMGLVGVYDPDSTPIGDASLTR 128
 DB 66 CIIKODMIIIRGTGNGCLLAQKPLDFGNAGALVGMVGPMKTTPIGDASLSKR 125
 OY 129 PMGRVLANPREGVGVKSESDGRLPTTLRGPKPTPTITRVPMASAOVKSAYVLAGLAMP 188
 DB 126 PMARILDPQLMGVEIEATHGVNLTLYGPKMTNICTRIPASAOVKSATILLAGLANTA 185
 OY 189 GTTIVIEPIITRDHTEKMLQGFGANLTVETDADGVITIRLEGKGLTGQVIDVPGDPSSST 248
 DB 186 GTTIVIEPIITRDHTEKMLKAFGAKLEIKNAAGTRFIHLNGHPLTGQTIHLPDPSA 245
 OY 249 APPVLAALLVPGSDVTILVLANPRTGILITLOEMGADIEVINPRLAGGEDVADLRVNS 308
 DB 246 APPVLAALLVPGSDVTILVLANPRTGILITLOEMGADIEVINPRLAGGEDVADLRVNS 305
 OY 309 STLKGTVPEDEBPASMIIDEYPILAFAAFAEGATVWNGLEELVKSSDRLSAVANGKLXN 368
 DB 306 STLKGTVPEDEBPASMIIDEYPILAFAAFAEGATVWNGLEELVKSSDRLSAVANGKLXN 365
 OY 369 GVDCEGETSLVVRGRPDGKIGNAGAAVATHTLDRILMSFLVGLVSENPVTVDATM 428
 DB 366 HYDCEGQDFLLVHGKSAKGLG---GVNTHTLDRILMSFLVGLVSENPVTVDATM 422
 OY 423 IATSPFPMDLNAGLGAKI 447
 DB 423 IATSPFPMDLNAGLGAKI 441

RESULT 11
 O6NDP4 PRELIMINARY; PRT; 445 AA.
 AC O6NDP4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19).
 GN Name=aroA; Ordered locus names=RPA0061;
 OS Rhodopseudomonas palustris.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodopseudomonas.
 OX NCBI_Taxid=1076;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CGA009 / ATCC BAA-98;
 RX PubMed=14704707; DOI=10.1038/nbt923;
 RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
 RA Land M.U., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
 RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Pires C.,
 RA Harrison F.H., Gibson J., Harwood C.S.;
 RT "Complete genome sequence of the metabolically versatile
 RT photosynthetic bacterium Rhodopseudomonas palustris".
 RL Nat. Biotechnol. 22:55-61 (2004).
 CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
 CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 CC sixth step.
 CC -1- SIMILARITY: Belongs to the EPSP synthase family.
 DR EMBL; BX572593; CAE2505.1; -
 DR GO; GO:0003866; F:3-phosphoshikimate 1-carboxyvinyltransferase. . .; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. . .; IEA.
 DR InterPro; IPR006264; AroA Ctransf.
 DR InterPro; IPR001986; EPSP_synth.
 DR Pfam; PF00275; EPSP_synthase; 1.
 DR ProDom; PD001867; EPSP_synthase; 1.
 DR TIGRFAMs; TIGR01356; aroA; 1.
 DR PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
 DR PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
 KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
 KW Complete proteome; Transferase.
 SQ SEQUENCE 445 AA; 46372 MW; C64A2896297F4B77 CRC64;

Query Match 54.7%; Score 1252.5; DB 2; Length 445;
 Best Local Similarity 59.5%; Pred. No. 6.1e-67;
 Matches 263; Conservative 52; Mismatches 116; Indels 11; Gaps 5;

OY 9 PATARKSSGLSGTVIRPGDKSISHRSFMFGGLASGETRTITGLLEGEDVINTGKAMQAMGA 68
 DB 9 PLQARKSGALHTAVPBGDKSISHRALIIGALAVGSTRISGLLEGEDVINTKAMALGA 68
 OY 69 RIRKEDGTTIIDGVNGGLAPAPLDPGNAATGCLTMGLVGVYDPDSTPIGDASLTR 127
 DB 69 KYERTGDCEMRVHGVGVAGFATPEAPLDGNGSGTGLMGAAGSPVIVATFDGASLSRS 128
 OY 128 PMGRVLANPREGVGVKSESDGRLPTTLRGPKPTPTITRVPMASAOVKSAYVLAGLAMP 186
 DB 129 PMGRVLANPREGVGVKSESDGRLPTTLRGPKPTPTITRVPMASAOVKSAYVLAGLAMP 188
 OY 187 TGTITVIEPIITRDHTEKMLQGFGANLTVETDADGV--RTIRLEGKGLTGQVIDVPGD 244
 DB 189 AGCITTVIAEASRDHTEMLQHFGA--TIVIEABEAKHAKISLTQPELRKAPVVPAD 246
 OY 245 PSTAFPLVALLVPGSDVTILVLANPRTGILITLOEMGADIEVINPRLAGGEDVADL 304
 DB 247 PSTAFPLVALLVPGSDVTILVLANPRTGILITLOEMGADIEVINPRLAGGEDVADL 306
 OY 305 RVRSSTLKGVTVPEDRAPSMIDEYPILAFAAFAEGATVWNGLEELRVESRSLVANG 364
 DB 307 RVRSSTLKGVTVPEDRAPSMIDEYPILAFAAFAEGATVWNGLEELRVESRSLVANG 366
 OY 365 LKLVGVDCEGETSLVVRGRPDGKIGNAGAAVATHTLDRILMSFLVGLVSENPVTVD 424
 DB 367 LRVNGVAVEIAGDDLVBEKGHVPG-----GGVVAHTHMDHRIAMSGLASLAKDKVTVTD 421
 OY 425 DATMTATSPFPMDLNAGLGAK 446
 DB 425 DATMTATSPFPMDLNAGLGAK 446

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DB      422 DTAFATSPDPVPMQRIGAE 443

RESULT 12
AC      AROA BRAJA      STANDARD;      PRT;      469 AA.
ID      _AROA BRAJA
AC      089WF2;
DT      10-OCT-2003 (Rel. 42, Created)
DT      10-OCT-2003 (Rel. 42, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
DE      enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPs).
GN      Name=aroA; OrderedLocustNames=blr0738;
OS      Bradyrhizobium japonicum.
OC      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC      Bradyrhizobiaceae; Bradyrhizobium.
OX      NCBI_TaxID=375;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=USDA 110;
RX      MEDLINE=22484998; PubMed=12597275;
RA      Kaneo T., Nakamura Y., Sato S., Minamisawa K., Uchiyama T.,
RA      Sasamoto S., Watanabe A., Ideawa K., Iriyuchi M., Kawashima K.,
RA      Kohara M., Matsunoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA      Tabata S.;
RT      "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT      Bradyrhizobium japonicum USDA110."
RL      DNA Res. 9:189-197(2002).
CC      -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC      phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC      -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC      sixth step.
CC      -1- SUBUNIT: Monomer (By similarity).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC      -1- SIMILARITY: Belongs to the EPSP synthase family.
CC      -----
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CC      -----
DR      EMBL; AF005937; BAC4603.1; -.
DR      HAMAP; MF_00210; -. 1.
DR      InterPro; IPR006264; AroA.
DR      InterPro; IPR001986; EPSP synth.
DR      Pfam; PF00275; EPSP synthase; 1.
DR      ProDom; PD001867; EPSP_synth; 1.
DR      PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
DR      PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
DR      KMW Aromatic amino acid biosynthesis; Complete proteome; Transferase.
SQ      SEQUENCE 469 AA; 48980 MW; DA55AA4F23BB85D5 CR64;

Query Match      53.7%; Score 1228.5; DB 1, Length 469;
Best Local Similarity 56.7%; Pred. No. 1.8e-65;
Matches 254; Conservative 60; Mismatches 127; Indels 7; Gaps 3;

OY      1 MHGASRPATARKSGSGTRIPGDKSISHSRFMGSLAGERRITGLGGEVINTG 60
DB      25 LHSQOPRLQSRANGPLTGKVRVPEDKSISRALLTGLAAGEFRISGLLEGEDVLTNA 84
OY      61 KAMQAMGARIRKECD-TWIIIDGVNGGLAPAPAPLDFGNATGCRITMGLVGVYDFDSTF 119
DB      85 KSMQALGASVERTGPFAMKVGQVGAFAQPKAALDFGSGGCRUVMKAVAGCPSIAVF 144
OY      120 IGDASLTRPKGRVNLNPLREMGVQYS-EDGRLPYTLTGKPTPTPTTYRVMPASQVKS 178
DB      145 DGDASIRSRPMRIIDPLEKMGARVVSCEGGRLLPLTLOGARDPLPTITKTVASQIKS 204
OY      179 AVLLAGLMTPTGTTTTEPIMTEDHTEKMLQGFGANLTVETDADGVRTTFLBERGLTGQV 238

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DB      205 AVLLAGLAPGTTTYIESEASRDHTEMLKHPGADITSTKSGQRRTTYVQPELHGAN 264

OY      239 IDVPDPSSTAFPIVLAALLVPGSDVTILNVLNMPRTGLITLTQEMGADIEVINRLAG 298
DB      265 VVVPADPSAAPPVVAALLIAGSDVLSVMTNPNFRLTGLFTTLRMGASIESEVRGADG 324
OY      299 EDVADLRSSSTLKGVTPEDRAPSMIDIEYPLIAVAAAFAGCATMNLLEIRVYESRL 358
DB      365 EPMQGLRVRASTLRKVEVPEPRAPSMIDIEYLVLAFAAGTITMRGLQELRVKESDRL 384
OY      369 SAVANGKLKNGVDCBEGESTLVVRGRPDGKIGNAGAAVATHLDRITAMSFVWGLVSE 418
DB      385 EATAEMLAVNGKVEVSSDDLVVQGRGHVPG-----GGTVATHMHRITAMSLVWGCASD 439
OY      419 NPVTVDATMTATSPPEFMDIMAGIGAK 446
DB      440 QGVTVDDTAFATSPDPFIPMWRISIGAE 467

RESULT 13
AC      AROA CAUCR      STANDARD;      PRT;      443 AA.
ID      _AROA CAUCR
AC      09A2H2;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      25-OCT-2004 (Rel. 45, Last annotation update)
DE      3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
DE      enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPs).
GN      Name=aroA; OrderedLocustNames=CC3589;
OS      Caulobacter crescentus.
OC      Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC      Caulobacteraceae; Caulobacter.
OX      NCBI_TaxID=155892;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ATCC 19089 / CB15;
RX      MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA      Nieren W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA      Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA      Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA      DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA      Kolonay J.F., Smit J., Craven M.B., Khoult H.M., Sherry J.,
RA      Berry K.J., Uetdeck T.R., Tran K., Wolf A.M., Yarnatovich J.J.,
RA      Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA      Fraser C.M.;
RT      "Complete genome sequence of Caulobacter crescentus."
RL      Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC      -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC      phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC      -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC      sixth step.
CC      -1- SUBUNIT: Monomer (By similarity).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC      -1- SIMILARITY: Belongs to the EPSP synthase family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL; AB006017; AAK25551.1; -.
DR      PIR; C87694; C87694.
DR      TIGR; CC3589; -.
DR      HAMAP; MF_00210; -. 1.
DR      InterPro; IPR006264; AroA.
DR      InterPro; IPR001986; EPSP synth.
DR      Pfam; PF00275; EPSP synthase; 1.
DR      ProDom; PD001867; EPSP synth; 1.
DR      TIGRFAMs; TIGR01356; aroA; 1.
DR      PROSITE; PS00104; EPSP_SYNTHASE_1; 1.

```

DR PROSITE; PS00865; EPSP_SYNTHASE_2; FALSE_NEG.
 KW Aromatic amino acid biosynthesis; Complete proteome; Transferase.
 SQ SEQUENCE 443 AA; 46075 MW; 458BA1463E10B6EC CRC64;

Query Match 49.6%; Score 1135; DB 1; Length 443;

Best Local Similarity 55.8%; Pred. No. 6,4e-60;
 Matches 251; Conservative 45; Mismatches 138; Indels 16; Gaps 6;

QY 2 LKASSRPTATKSSGLSGTVRIIPGDKSISHRSFMFGASGETRTTGLLEGEDVINTK 61
 DB 3 LKGLKSAFAGG-----LRGIVRAPGDKSISHRSMTIGALLTGTVEGLLEGDDVATNR 57
 QY 62 AMQAGARIRKESG-DTWIIDGVNGGLLAPAPLDPGNAATGRLTMGLVGYVDPDSTPI 120
 DB 58 AMQAGARIRERGVGWRIE--GKGFEPPVDVDDGNGMTGRLTMGAAGRAMCATFT 115
 QY 121 GNASLTRPMGRVLANPLREMGVQVKSSEDGRLPVTLRGPKTPPTTYRVPMASQVKSAY 180
 DB 116 GPQSLRGPMGRVLDPLAMGATWLCGRDKGRPLTLTKGNL--RGLNYTLPMASQVKSAY 174
 QY 181 LLAGNTPGITTYIEPIMTDHEKMLQGRGANLTVETDADGVRT--IRLEGKLTGQ 237
 DB 175 LLAGLHABEGVEYTEBATRDHTRMLRAFGAEVIEDRKAGDKTRHVRRLPEGQKLTGT 234
 QY 238 VIDVPGDPSTAPFLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAG 297
 DB 235 HYAVPDPSSAFLVVAALIVPSEVTVGVMLEARTGLFTLQEMGADIVISNVRVAS 294
 QY 298 GEDVADLRVRSSTLKGVTVPEDRAPSMIDEPYLAVAAPFAGATVMNGLEELRYKESDR 357
 DB 295 GEVEGDITARYSLQKGVVPPERAPSMIDEPYLAVAAPFAGATVMNGLEELRYKESDR 354
 QY 358 LEAVNGLKLVNDCEGETSLVVRGRPDGKLGNAAGAAVATHLDHRIAMSTLVNGLYS 417
 DB 355 ISLTANGLACGVQVVEEPEGFLV---TGTGQPPKGAITVYHGHRIAMSHLILGMGA 410
 QY 418 ENPVTVDATMTATSPPEFMDLMAGLAKI 447
 DB 411 QAEVAVDERGMTATSPFGADLMRGIGATL 440

RESULT 14

Q9H269 PRELIMINARY; PRT; 746 AA.

AC 09H269; 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Still frameshift 3-PHOSPHOSHIMIMATE 1-CARBOXYVINYLTRANSFERASE
 DE prephenate dehydrogenase.
 GN OrderedlocusNames=PA3164;
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxId=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mikooguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kae A., Larbig K.T., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V., an
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen.";
 RT Nature 406:959-964(2000).
 CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
 CC phosphatate + 5-O-(1-carboxyviny)l-3-phosphoshikimate.
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 CC sixth step.
 CC -1- SIMILARITY: Belongs to the EPSP synthase family.

DR EMBL; AE004740; AA06552.1; --
 DR PIR; B83250; B83250.
 DR HSSP; Q9S400; 1RP4.
 DR GO; GO:0003866; F:3-phosphoshikimate-1-carboxyvinyltrnsferase; .; IEA.
 DR GO; GO:0004665; F:prephenate dehydrogenase (NADP+) activity; IEA.
 DR GO; GO:0016740; F:transferrase activity; IEA.
 DR GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. .; IEA.
 DR GO; GO:0006571; P:tyrosine biosynthesis; IEA.
 DR InterPro; IPR006264; AroC_Ctransf.
 DR InterPro; IPR001986; EPSP_synth.
 DR InterPro; IPR000205; NAD_BS.
 DR InterPro; IPR003099; Prephen_dehydrog.
 DR Pfam; PF00275; EPSP_synthase; 1.
 DR Prodom; PD001867; EPSP synth; 1.
 DR TIGRfam; TIGR01356; atoa; 1.
 DR PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
 DR PROSITE; PS00865; EPSP_SYNTHASE_2; 1.
 KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
 KW Complete proteome; Transferase.
 SQ SEQUENCE 746 AA; 79320 MW; C297484BF539E3A CRC64;

Query Match 43.2%; Score 989.5; DB 2; Length 746;
 Best Local Similarity 48.5%; Pred. No. 5.9e-51;
 Matches 214; Conservative 62; Mismatches 152; Indels 13; Gaps 3;

QY 12 ARKSSGLSGTVRIIPGDKSISHRSFMFGASGETRTTGLLEGEDVINTKAMQAGARIR 71
 DB 317 AOPGSLSGTIRVPGDKSISHRSIMGLSABGTTEVEGLLEGEDALATTQAFDMGVYIE 376
 QY 72 -KEGDWIIDGVNGGLLAPAPLDPGNAATGRLTMGLVGYVDPDSTPIGASLTRKPM 130
 DB 377 GPQNGNVTVHGVGLKAPRPGPIYVNGSTGMRLLSGLLAQPFPSTLIGDASLSKRM 436
 QY 131 GRVNLPRMGVQVKSSEDGRLPVTLRGPKTPPTTYRVPMASQVKSAYVLAAGLTPGI 190
 DB 437 NRVAKPLREMGAVIEGPEGRPMITRGQRLTGKMHYDPMASQVKSCLLALGLYAAE 496
 QY 191 TVIPIPIMTDHEKMLQGRGANLTVETDADGVRTIRLEGKLTGQVLDVDPDSTAP 250
 DB 497 TSVTEPAPTRDHTERMLRGFGYPVVEGS-----TAKVSGHLSKTHLEVPADISSAF 551
 QY 251 PLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGEDVADLRVRSST 310
 DB 552 FLVAASIAEGSELVQHGVINPTRGVIEILLMGSDLSLEQREVGSGRPVADIRRSAR 611
 QY 311 LKGVTVPEDRAPSMIDEPYLAVAAPFAGATVMNGLEELRYKESDRLSAVANGKLNGV 370
 DB 612 LKSIDIPEDLVLAIDEPFVLVFAAACAGERTVLRGAELRYKESDRIOVMADGLKALGV 671
 QY 371 DCDDEGETSLVVRGRPDGKLGNAAGAAVATHLDHRIAMSTLVNGLYSENPVTVDDATMTA 430
 DB 672 KAEPTPDGIVIG-----GAFGGGEVNAHGDHRIAMSFVASLRSASGPIRHHDCANVA 724
 QY 431 TSPPEFMDLMAGLAKIELSD 451
 DB 725 TSPPNFLALCAQTGRVAVEN 745

RESULT 15

Q88M05 PRELIMINARY; PRT; 746 AA.

AC 088M05; 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Prephenate dehydrogenase, putative/3-phosphoshikimate 1-
 DE carboxyvinyltrnsferase.
 GN OrderedlocusNames=pl1770;
 OS Pseudomonas putida (strain KT2440).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxId=160488;

RN SEQUENCE FROM N.A.
 [1]
 RX MEDLINE=22423060; PubMed=12534463;
 RA Nelson K.E., Meinel C., Paulsen I.T., Dodson R.J., Pop M., Holmes M.,
 RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Holmes M.,
 RA Brinkup L.M., Beaman M.J., Deboy R.T., Daugherty S.C., Kolonay J.F.,
 RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
 RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
 RA Moszzer A., Utterback T.R., Rizzo M., Lee K., Kosack D., Mostl D.,
 RA Weller H., Lauber J., Stjepandic D., Hohnsbeil U., Streletz M., Helm S.,
 RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tnemmler B.,
 RA Fraser C.M.,
 RT "Complete genome sequence and comparative analysis of the
 RT metabolically versatile *Pseudomonas putida* KT2440.";
 RL Environ. Microbiol. 4:799-808(2002).
 CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphohikimate =
 CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphohikimate.
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 CC sixth step.
 CC -1- SIMILARITY: Belongs to the EPSP synthase family.
 DR EMBL; AE016780; AA067390.1; --
 DR HSSP; Q9S400; IRP4.
 DR TIGR; PP1770; --
 DR GO; GO:0003866; F:3-phosphohikimate 1-carboxyvinyltransferase. .; IEA.
 DR GO; GO:0004665; F:prephenate dehydrogenase (NADP+) activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0016089; F:aromatic amino acid family biosynthesis, sh. .; IEA.
 DR GO; GO:0006571; P:tyrosine biosynthesis; IEA.
 DR InterPro; IPR006264; Arco_Ctransf.
 DR InterPro; IPR001986; EPSP synth.
 DR InterPro; IPR000205; NAD BS.
 DR InterPro; IPR001099; prephen_dhydrog.
 DR Pfam; PF00275; EPSP_synthase; 1.
 DR Pfam; PF02153; PDH; 1.
 DR PRODOM; PD001867; EPSP_synth; 1.
 DR TIGRFAMs; TIGR01356; arco; 1.
 DR PROSITE; PS00104; EPSP SYNTHASE_1; 1.
 DR PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
 KW amino-acid biosynthesis; Aromatic amino acid biosynthesis;
 KW Complete proteome; Transferase.
 KW SEQUENCE 746 AA; 79133 MW; 7148AA1B4DDC1AB2 CRC64;
 SQ
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 Best Local Similarity 49.2%; Pred. No. 8e-50;
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Search completed: April 20, 2005, 15:25:56
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Search completed: April 20, 2005, 15:25:50
Job time : 75 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 20, 2005, 15:23:22 ; Search time 139 Seconds
(without alignments)
1087.976 Million cell updates/sec

Title: US-10-622-201-70
Perfect score: 2288
Sequence: 1.MHGASRRPARKSSGLSG.....FMDIAGIGAKITLSDTYKA 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues
Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2288	100.0	455	9	US-09-861-696-70 Sequence 70, Appl
2	2288	100.0	455	9	US-09-464-099A-70 Sequence 70, Appl
3	2282	99.7	455	9	US-09-861-696-3 Sequence 3, Appl
4	2282	99.7	455	9	US-09-464-099A-3 Sequence 3, Appl
5	2271	99.3	524	15	US-10-424-599-169346 Sequence 169346, Appl
6	1900.5	83.1	449	9	US-09-861-696-5 Sequence 5, Appl
7	1900.5	83.1	449	9	US-09-861-696-7 Sequence 7, Appl
8	1900.5	83.1	449	9	US-09-464-099A-5 Sequence 5, Appl
9	1900.5	83.1	449	9	US-09-464-099A-7 Sequence 7, Appl
10	1853.5	81.1	480	14	US-10-214-766-30 Sequence 30, Appl
11	1783	77.9	452	15	US-10-369-493-12116 Sequence 12116, A
12	1233.5	53.9	430	15	US-10-369-493-20766 Sequence 20766, A
13	1213.5	53.0	432	15	US-10-369-493-10476 Sequence 10476, A

14	1188.5	51.9	418	15	US-10-369-493-7814 Sequence 7814, Ap
15	1149.5	50.2	440	15	US-10-369-493-18039 Sequence 18039, A
16	1135	49.6	423	15	US-10-369-493-17074 Sequence 17074, A
17	983	43.0	411	15	US-10-369-493-9974 Sequence 9974, Ap
18	927.5	40.5	442	15	US-10-369-493-15383 Sequence 15383, A
19	912.5	39.9	454	15	US-10-369-493-17730 Sequence 17730, A
20	908.5	39.7	408	15	US-10-369-493-9302 Sequence 9302, Ap
21	908.5	39.7	412	15	US-10-369-493-9499 Sequence 9499, Ap
22	906.5	39.6	408	15	US-10-369-493-15751 Sequence 15751, A
23	906.5	39.6	408	15	US-10-369-493-16135 Sequence 16135, A
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27	867.5	37.9	447	15	US-09-464-099A-67 Sequence 67, Appl
28	867.5	37.9	447	15	US-10-369-493-2764 Sequence 2764, Ap
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32	806	35.2	443	9	US-09-861-696-69 Sequence 69, Appl
33	806	35.2	443	9	US-09-464-099A-69 Sequence 69, Appl
34	806	35.2	443	14	US-10-214-766-31 Sequence 31, Appl
35	803.5	35.1	417	15	US-10-369-493-16494 Sequence 16494, A
36	803.5	35.1	427	17	US-10-472-928-2780 Sequence 2780, Ap
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39	785	34.3	428	9	US-09-464-099A-42 Sequence 42, Appl
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43	577	25.2	430	9	US-09-861-696-44 Sequence 44, Appl
44	577	25.2	430	9	US-09-464-099A-44 Sequence 44, Appl
45	521.5	22.8	429	15	US-10-335-977-6495 Sequence 6495, Ap

ALIGNMENTS

RESULT 1
US-09-861-696-70
Sequence 70, Application US/09861696
Patent No. US20020007053A1
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES
FILE REFERENCE: 11899, 0175, CUS04 MOBT:175-4
CURRENT APPLICATION NUMBER: US/09/861,696
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/137,440
PRIOR FILING DATE: 1998-08-20
PRIOR APPLICATION NUMBER: US 08/833,485
PRIOR FILING DATE: 1997-04-07
PRIOR APPLICATION NUMBER: US 08/306,063
PRIOR FILING DATE: 1994-09-13
PRIOR APPLICATION NUMBER: US 07/749,611
PRIOR FILING DATE: 1991-08-28
PRIOR APPLICATION NUMBER: US 07/576,537
PRIOR FILING DATE: 1990-08-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.0
SEQ ID NO 70
LENGTH: 455
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-861-696-70
Query Match 100.0%; Score 2288; DB 9; Length 455;
Best Local Similarity 100.0%; Pred. No. 7.4e-182;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 361 VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAATAVTHLDRIRIAMSFLVMGLVSENP 420
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RESULT 2
US-09-464-099A-70
; Sequence 70, Application US/09464099A
; Patent No. US20020168680A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOPLPYUVULSHIKIMATE-3-PHOSPHATE SYNTHASES
; FILE REFERENCE: 11899.0175.CNDS01 MOBT:175-2
; CURRENT APPLICATION NUMBER: US/09/464,099A
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/137,440
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 08/833,485
; PRIOR FILING DATE: 1997-04-07
; PRIOR APPLICATION NUMBER: US 08/306,063
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 07/749,611
; PRIOR FILING DATE: 1991-08-28
; PRIOR APPLICATION NUMBER: US 07/576,537
; PRIOR FILING DATE: 1990-08-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 70
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-464-099A-70

Query Match 100.0%; Score 2288; DB 9; Length 455;
Best Local Similarity 100.0%; Pred. No. 7.4e-182;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
US-09-861-696-3
; Sequence 3, Application US/09861696
; Patent No. US20020007053A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOPLPYUVULSHIKIMATE-3-PHOSPHATE SYNTHASES
; FILE REFERENCE: 11899.0175.CNDS04 MOBT:175-4
; CURRENT APPLICATION NUMBER: US/09/861,696
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/137,440
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 08/833,485
; PRIOR FILING DATE: 1997-04-07
; PRIOR APPLICATION NUMBER: US 08/306,063
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 07/749,611
; PRIOR FILING DATE: 1991-08-28
; PRIOR APPLICATION NUMBER: US 07/576,537
; PRIOR FILING DATE: 1990-08-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 455
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; ORGANISM: Agrobacterium sp.
US-09-861-696-3

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Best Local Similarity 99.8%; Pred. No. 2.3e-181;
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; Patent No. US20020168680A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOPIRYVUVYSHIKIMATE-3-PHOSPHATE SYNTHASES
; FILE REFERENCE: 11899, 0175, CINTS01 MOST:175-2
; CURRENT APPLICATION NUMBER: US/09/464, 099A
; CURRENT FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/137, 440
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 08/833, 485
; PRIOR FILING DATE: 1997-04-07
; PRIOR APPLICATION NUMBER: US 08/306, 063
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 07/749, 611
; PRIOR FILING DATE: 1991-08-28
; PRIOR APPLICATION NUMBER: US 07/576, 537
; PRIOR FILING DATE: 1990-08-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRY
; ORGANISM: Agrobacterium sp.
US-09-464-099A-3

Query Match 99.7%; Score 2282; DB 9; Length 455;
Best Local Similarity 99.8%; Pred. No. 2,3e-181;
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MHGASSRPATARKSSGSLGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60
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DB 61 KAMQAMGARIRKEDGTWIIDGVNGGLAPEAPLDFGNATGRLTMGLVGVDPDSTFI 120
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DB 121 GDSATKCPMGVNLPLREMGVQVKSSEDGRLPVTLRGKPTPTITRYVPMASAOVKSAY 180
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DB 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFANLTVETDADGVRTIRLEGKGLTGQVID 240
QY 241 VPGDSSSTAFPLVAALLVPGSDVTTILNVLNMPTRGILLTLOMGADIEVINPRLAGSD 300
DB 241 VPGDSSSTAFPLVAALLVPGSDVTTILNVLNMPTRGILLTLOMGADIEVINPRLAGSD 300
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DB 361 VANGKLKLVGDCDEGETSLVVRGPRDGKGLGNASGAAVAATHLDRHJAMSLVWGLVSENP 420

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DB 241 VPGDSSSTAFPLVAALLVPGSDVTTILNVLNMPTRGILLTLOMGADIEVINPRLAGSD 300
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DB 421 VTVDATMTATSPPEFMDLMAGLGAKIELSDTKAA 455

RESULT 5

US-10-424-599-169346
; Sequence 169346, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424, 599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 169346
; LENGTH: 524
; TYPE: PRY
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: PAT_MRT3847_123934C.1.dep
US-10-424-599-169346

Query Match 99.3%; Score 2271; DB 15; Length 524;
Best Local Similarity 99.8%; Pred. No. 2,4e-180;
Matches 451; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHGASSRPATARKSSGSLGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60
DB 1 MHGASSRPATARKSSGSLGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60
QY 61 KAMQAMGARIRKEDGTWIIDGVNGGLAPEAPLDFGNATGRLTMGLVGVDPDSTFI 120
DB 61 KAMQAMGARIRKEDGTWIIDGVNGGLAPEAPLDFGNATGRLTMGLVGVDPDSTFI 120
QY 121 GDSATKCPMGVNLPLREMGVQVKSSEDGRLPVTLRGKPTPTITRYVPMASAOVKSAY 180
DB 121 GDSATKCPMGVNLPLREMGVQVKSSEDGRLPVTLRGKPTPTITRYVPMASAOVKSAY 180
QY 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFANLTVETDADGVRTIRLEGKGLTGQVID 240
DB 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFANLTVETDADGVRTIRLEGKGLTGQVID 240
QY 241 VPGDSSSTAFPLVAALLVPGSDVTTILNVLNMPTRGILLTLOMGADIEVINPRLAGSD 300
DB 241 VPGDSSSTAFPLVAALLVPGSDVTTILNVLNMPTRGILLTLOMGADIEVINPRLAGSD 300
QY 301 VADLRVRSSTLKGVTVPEDRAPSMIDEYPIILVAAAFAGATVMNGLEELRYKESDRLSA 360
DB 301 VADLRVRSSTLKGVTVPEDRAPSMIDEYPIILVAAAFAGATVMNGLEELRYKESDRLSA 360
QY 361 VANGKLKLVGDCDEGETSLVVRGPRDGKGLGNASGAAVAATHLDRHJAMSLVWGLVSENP 420
DB 361 VANGKLKLVGDCDEGETSLVVRGPRDGKGLGNASGAAVAATHLDRHJAMSLVWGLVSENP 420

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Db 433 VANGKJNGVDCDEBETSLVVRGRPDGKLGNAAGVATLHDRIANSFLVNGLVSENP 492
Qy 421 VTVDATMIATSFPEFMDMAGLGAKEIISDT 452
Db 493 VTVDATMIATSFPEFMDMAGLGAKEIISDT 524

RESULT 6
US-09-861-696-5
; Sequence 5, Application US/09861696
; Patent No. US20020007053A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOPIRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES
; FILE REFERENCE: 11899.0175.CNUS04 MOBT:175-4
; CURRENT APPLICATION NUMBER: US/09/861,696
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/137,440
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 08/833,485
; PRIOR FILING DATE: 1997-04-07
; PRIOR APPLICATION NUMBER: US 08/306,063
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 07/749,611
; PRIOR FILING DATE: 1991-08-28
; PRIOR APPLICATION NUMBER: US 07/576,537
; PRIOR FILING DATE: 1990-08-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Agrobacterium sp.
US-09-861-696-5

Query Match 83.1%; Score 1900.5; DB 9; Length 449;
Best Local Similarity 82.9%; Pred. No. 1.4e-149;
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

Qy 1 MHHGSSRPATARKSSGLSGTVIRIPGDKSISHSRSMFGLASGETRITGLLEGEDVINTG 60
Db 1 MSHSASPPKATRRSEALTGIRIPGDKSISHSRSMFGLASGETRITGLLEGEDVINTG 60
Qy 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPPEALPDGNAATGCRITMGLVGYDDPSFTI 120
Db 61 RAMQAMGAKIRKEGDTWIIDGVNGGLAPPEALPDGNAATGCRITMGLVGYDDPSFTI 120
Qy 121 GDASLTKEPMGRVNLPLREMGVQVXSEBDRLPVLTRGPXTPTPTTYRVPMASQVKSAY 180
Db 121 GDASLTKEPMGRVNLPLREMGVQVXSEBDRLPVLTRGPXTPTPTTYRVPMASQVKSAY 180
Qy 121 GDASLTKEPMGRVNLPLREMGVQVXSEBDRLPVLTRGPXTPTPTTYRVPMASQVKSAY 180
Db 121 GDASLTKEPMGRVNLPLREMGVQVXSEBDRLPVLTRGPXTPTPTTYRVPMASQVKSAY 180
Qy 181 LLAGINTPGITTVIPIRMDRTEKMLQCFGANLTVETDADGVRTIRLEGKGLTGQVID 240
Db 181 LLAGINTPGITTVIPIRMDRTEKMLQCFGANLTVETDADGVRTIRLEGKGLTGQVID 240
Qy 241 VPGDSSSTAFPLVALLVPGSDVTILNVLNMPTRTGLITLQEMGADIEVINPRLAGGED 300
Db 241 VPGDSSSTAFPLVALLVPGSDVTILNVLNMPTRTGLITLQEMGADIEVINPRLAGGED 300
Qy 301 VADLRVRSSTLKGVVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLEELRYKESDRLSA 360
Db 301 VADLRVRSSTLKGVVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLEELRYKESDRLSA 360
Qy 361 VANGKJNGVDCDEBETSLVVRGRPDGKLGNAAGVATLHDRIANSFLVNGLVSENP 420
Db 361 VANGKJNGVDCDEBETSLVVRGRPDGKLGNAAGVATLHDRIANSFLVNGLVSENP 420
Qy 421 VTVDATMIATSFPEFMDMAGLGAKEIIS 450
Db 421 VTVDATMIATSFPEFMDMAGLGAKEIIS 450
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Db 418 VTVDSSNMIAATSFPEFMDMAGLGAKEIIS 447
Qy 418 VTVDSSNMIAATSFPEFMDMAGLGAKEIIS 447

RESULT 7
US-09-861-696-7
; Sequence 7, Application US/09861696
; Patent No. US20020007053A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOPIRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES
; FILE REFERENCE: 11899.0175.CNUS04 MOBT:175-4
; CURRENT APPLICATION NUMBER: US/09/861,696
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/137,440
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 08/833,485
; PRIOR FILING DATE: 1997-04-07
; PRIOR APPLICATION NUMBER: US 08/306,063
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 07/749,611
; PRIOR FILING DATE: 1991-08-28
; PRIOR APPLICATION NUMBER: US 07/576,537
; PRIOR FILING DATE: 1990-08-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Pseudomonas sp.
US-09-861-696-7

Query Match 83.1%; Score 1900.5; DB 9; Length 449;
Best Local Similarity 82.9%; Pred. No. 1.4e-149;
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

Qy 1 MHHGSSRPATARKSSGLSGTVIRIPGDKSISHSRSMFGLASGETRITGLLEGEDVINTG 60
Db 1 MSHSASPPKATRRSEALTGIRIPGDKSISHSRSMFGLASGETRITGLLEGEDVINTG 60
Qy 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPPEALPDGNAATGCRITMGLVGYDDPSFTI 120
Db 61 RAMQAMGAKIRKEGDTWIIDGVNGGLAPPEALPDGNAATGCRITMGLVGYDDPSFTI 120
Qy 121 GDASLTKEPMGRVNLPLREMGVQVXSEBDRLPVLTRGPXTPTPTTYRVPMASQVKSAY 180
Db 121 GDASLTKEPMGRVNLPLREMGVQVXSEBDRLPVLTRGPXTPTPTTYRVPMASQVKSAY 180
Qy 121 GDASLTKEPMGRVNLPLREMGVQVXSEBDRLPVLTRGPXTPTPTTYRVPMASQVKSAY 180
Db 121 GDASLTKEPMGRVNLPLREMGVQVXSEBDRLPVLTRGPXTPTPTTYRVPMASQVKSAY 180
Qy 181 LLAGINTPGITTVIPIRMDRTEKMLQCFGANLTVETDADGVRTIRLEGKGLTGQVID 240
Db 181 LLAGINTPGITTVIPIRMDRTEKMLQCFGANLTVETDADGVRTIRLEGKGLTGQVID 240
Qy 241 VPGDSSSTAFPLVALLVPGSDVTILNVLNMPTRTGLITLQEMGADIEVINPRLAGGED 300
Db 241 VPGDSSSTAFPLVALLVPGSDVTILNVLNMPTRTGLITLQEMGADIEVINPRLAGGED 300
Qy 301 VADLRVRSSTLKGVVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLEELRYKESDRLSA 360
Db 301 VADLRVRSSTLKGVVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLEELRYKESDRLSA 360
Qy 361 VANGKJNGVDCDEBETSLVVRGRPDGKLGNAAGVATLHDRIANSFLVNGLVSENP 420
Db 361 VANGKJNGVDCDEBETSLVVRGRPDGKLGNAAGVATLHDRIANSFLVNGLVSENP 420
Qy 421 VTVDATMIATSFPEFMDMAGLGAKEIIS 450
Db 421 VTVDATMIATSFPEFMDMAGLGAKEIIS 450
Qy 418 VTVDSSNMIAATSFPEFMDMAGLGAKEIIS 447
Db 418 VTVDSSNMIAATSFPEFMDMAGLGAKEIIS 447

RESULT 8
US-09-464-099A-5
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; Sequence 5, Application US/09464099A
; Patent No. US20020168680A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES
; FILE REFERENCE: 11899.0175.CNISO1 MOBT:175-2
; CURRENT APPLICATION NUMBER: US/09/464,099A
; CURRENT FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/137,440
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 08/833,485
; PRIOR FILING DATE: 1997-04-07
; PRIOR APPLICATION NUMBER: US 08/306,063
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 07/749,611
; PRIOR FILING DATE: 1991-08-28
; PRIOR APPLICATION NUMBER: US 07/576,537
; PRIOR FILING DATE: 1990-08-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Agrobacterium sp.
US-09-464-099A-5
```

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Query Match      83.1%; Score 1900.5; DB 9; Length 449;
Best Local Similarity 82.9%; Pred. No. 1.4e-149;
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;
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QY      1 MHGASSRPATARKSSGSLGTVRIPGDKSISHRSEFMFGGLASGETRTITGLBSEEDYINTG 60
DB      1 MSHSASPKPATARRSALTEIRIPGDKSISHRSEFMFGGLASGETRTITGLBSEEDYINTG 60
QY      61 KAMQAMGAKIRKRGDWTIIDVNGGGLAPAPLDPGNATGCRITMGLVGVDPFSTFI 120
DB      61 RAMQAMGAKIRKRGDWTIIDVNGGGLAPAPLDPGNATGCRITMGLVGVDPFSTFI 120
QY      121 GDSILTKRPMGRVNLPLREMGVQVKSDEGDRPLVTLRGPKTPPTITRYVPMASQVKSAY 180
DB      121 GDSILTKRPMGRVNLPLREMGVQVKSDEGDRPLVTLRGPKTPPTITRYVPMASQVKSAY 180
QY      121 GDSILTKRPMGRVNLPLREMGVQVKSDEGDRPLVTLRGPKTPPTITRYVPMASQVKSAY 180
DB      121 GDSILTKRPMGRVNLPLREMGVQVKSDEGDRPLVTLRGPKTPPTITRYVPMASQVKSAY 180
QY      181 LLAGLNTPGITTYIEPIWTRDHTKMLQGFANLTYETDADGVRTIRLBGRKLTQVTD 240
DB      181 LLAGLNTPGITTYIEPIWTRDHTKMLQGFANLTYETDADGVRTIRLBGRKLTQVTD 240
QY      241 VPGDPESTAFPLVAALLVGSQVTLINVLNMPRTGILITLOEMGADIEVINRLAGGED 300
DB      241 VPGDPESTAFPLVAALLVGSQVTLINVLNMPRTGILITLOEMGADIEVINRLAGGED 300
QY      301 VADLRVRSSTLKGVTPEDRAPSMIDEPYLAFAAGATVMNGLEELRVKESDRLSA 360
DB      301 VADLRVRSSTLKGVTPEDRAPSMIDEPYLAFAAGATVMNGLEELRVKESDRLSA 360
QY      301 VADLRVRSSTLKGVTPEDRAPSMIDEPYLAFAAGATVMNGLEELRVKESDRLSA 360
DB      301 VADLRVRSSTLKGVTPEDRAPSMIDEPYLAFAAGATVMNGLEELRVKESDRLSA 360
QY      361 VANGELKLVGDCDEGETSLVVRGRPDGKIGNAGAAVATHLDHRIAMSLVNLVSENP 420
DB      361 VANGELKLVGDCDEGETSLVVRGRPDGKIGNAGAAVATHLDHRIAMSLVNLVSENP 420
QY      421 VVYDDATMTATSPPEFMDMAGIGAKIELS 450
DB      421 VVYDDATMTATSPPEFMDMAGIGAKIELS 450
QY      418 VVYDDSNMTATSPPEFMDMAGIGAKIELS 447
DB      418 VVYDDSNMTATSPPEFMDMAGIGAKIELS 447
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RESULT 9
US-09-464-099A-7
; Sequence 7, Application US/09464099A
; Patent No. US20020168680A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
```

```
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES
; FILE REFERENCE: 11899.0175.CNISO1 MOBT:175-2
; CURRENT APPLICATION NUMBER: US/09/464,099A
; CURRENT FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/137,440
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 08/833,485
; PRIOR FILING DATE: 1997-04-07
; PRIOR APPLICATION NUMBER: US 08/306,063
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 07/749,611
; PRIOR FILING DATE: 1991-08-28
; PRIOR APPLICATION NUMBER: US 07/576,537
; PRIOR FILING DATE: 1990-08-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Pseudomonas sp.
US-09-464-099A-7
```

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Query Match      83.1%; Score 1900.5; DB 9; Length 449;
Best Local Similarity 82.9%; Pred. No. 1.4e-149;
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;
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QY      1 MHGASSRPATARKSSGSLGTVRIPGDKSISHRSEFMFGGLASGETRTITGLBSEEDYINTG 60
DB      1 MSHSASPKPATARRSALTEIRIPGDKSISHRSEFMFGGLASGETRTITGLBSEEDYINTG 60
QY      61 KAMQAMGAKIRKRGDWTIIDVNGGGLAPAPLDPGNATGCRITMGLVGVDPFSTFI 120
DB      61 RAMQAMGAKIRKRGDWTIIDVNGGGLAPAPLDPGNATGCRITMGLVGVDPFSTFI 120
QY      121 GDSILTKRPMGRVNLPLREMGVQVKSDEGDRPLVTLRGPKTPPTITRYVPMASQVKSAY 180
DB      121 GDSILTKRPMGRVNLPLREMGVQVKSDEGDRPLVTLRGPKTPPTITRYVPMASQVKSAY 180
QY      121 GDSILTKRPMGRVNLPLREMGVQVKSDEGDRPLVTLRGPKTPPTITRYVPMASQVKSAY 180
DB      121 GDSILTKRPMGRVNLPLREMGVQVKSDEGDRPLVTLRGPKTPPTITRYVPMASQVKSAY 180
QY      181 LLAGLNTPGITTYIEPIWTRDHTKMLQGFANLTYETDADGVRTIRLBGRKLTQVTD 240
DB      181 LLAGLNTPGITTYIEPIWTRDHTKMLQGFANLTYETDADGVRTIRLBGRKLTQVTD 240
QY      241 VPGDPESTAFPLVAALLVGSQVTLINVLNMPRTGILITLOEMGADIEVINRLAGGED 300
DB      241 VPGDPESTAFPLVAALLVGSQVTLINVLNMPRTGILITLOEMGADIEVINRLAGGED 300
QY      301 VADLRVRSSTLKGVTPEDRAPSMIDEPYLAFAAGATVMNGLEELRVKESDRLSA 360
DB      301 VADLRVRSSTLKGVTPEDRAPSMIDEPYLAFAAGATVMNGLEELRVKESDRLSA 360
QY      301 VADLRVRSSTLKGVTPEDRAPSMIDEPYLAFAAGATVMNGLEELRVKESDRLSA 360
DB      301 VADLRVRSSTLKGVTPEDRAPSMIDEPYLAFAAGATVMNGLEELRVKESDRLSA 360
QY      361 VANGELKLVGDCDEGETSLVVRGRPDGKIGNAGAAVATHLDHRIAMSLVNLVSENP 420
DB      361 VANGELKLVGDCDEGETSLVVRGRPDGKIGNAGAAVATHLDHRIAMSLVNLVSENP 420
QY      421 VVYDDATMTATSPPEFMDMAGIGAKIELS 450
DB      421 VVYDDATMTATSPPEFMDMAGIGAKIELS 450
QY      418 VVYDDSNMTATSPPEFMDMAGIGAKIELS 447
DB      418 VVYDDSNMTATSPPEFMDMAGIGAKIELS 447
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RESULT 10
US-10-214-766-30
; Sequence 30, Application US/10214766
; Publication No. US20030084473A1
; GENERAL INFORMATION:
; APPLICANT: Gocal, Greg
; TITLE OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT PLANTS
; FILE REFERENCE: CA1138
; CURRENT APPLICATION NUMBER: US/10/214,766
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,734
; PRIOR FILING DATE: 2001-08-09
```

NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.2
SEQ ID NO 30
LENGTH: 480
TYPE: PRF
ORGANISM: Brucella melitensis
NAME/KEY: misc_feature
LOCATION: (364)..(364)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-214-766-30

Query Match 81.1%; Score 1855.5; DB 14; Length 480;
Best Local Similarity 81.4%; Pred. No. 8.3e-146;

Matches 364; Conservative 35; Mismatches 45; Indels 3; Gaps 1;

QY 1 MLHGASRPATARKSGSGTIRIPGDKSISHRSPFGGLASGERTITGLLEGEDVINTG 60
DB 31 MSHSACPATARKSGLTGEIRIPGDKSISHRSPFGGLASGERTITGLLEGEDVINTG 90
QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLPDFGNAATGCRITMGLVGVYDPDSTFI 120
DB 91 RAMQAMGARIRKEGDTWIIDGVNGGLAPAPLPDFGNAATGCRITMGLVGVYDPDSTFI 150
QY 121 GPASLTGRPMGVNPLREMGVQV-KSEDDRLPYTLRGKPTPTPTTYRVPMAAQVKSAY 180
DB 151 GPASLSKRMGVNPLREMGVQVEABEDRMPPLTIGPRITANPLAVRVPMAAQVKSAY 210
QY 181 LLAGLNTPGITTVIEPMTDHEKMLQSGANLTVETDADGVRTIRLEGKLTGQVTD 240
DB 211 LLAGLNTPGITTVIEPMTDHEKMLQSGADLTVEITKQVGRHRIIVGQKLTGQVTD 270
QY 241 VEGDPSSTAFPLVAALVPGSDVTILNVLNMPRTGLITLQEMGADIEVINPRLAGSD 300
DB 271 VEGDPSSTAFPLVAPLVGSEVTVIRNVLMNPTRTGLITLQEMGADIEVINPRLAGSD 330
QY 301 VADLRVRSSTLKGTVPEBRAPSMIDEPYLAFAAGATVNGLEIRVKSDELISA 360
DB 331 VADLRVRSSTLKGTVPEBRAPSMIDEPYLAFAAGATVNGLEIRVKSDELISA 390
QY 361 VANGKLKNGVDCDEGETSLVVRGPRDGKGLGNASGAATVTHDHRIRMSFLVMGLV 420
DB 391 VANGKLKNGVDCDEGETSLVVRGPRDGKGLGNASGAATVTHDHRIRMSFLVMGLV 447
QY 421 VTVDATMTATSPPEFMDLMAIGAKI 447
DB 448 VTVDSTMTATSPPEFMDLMAIGAKI 474

RESULT 11

US-10-369-493-12116

Sequence 12116, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

FILE REFERENCE: 38-10(52052)B

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 12116

LENGTH: 452

TYPE: PRF

ORGANISM: Mesorhizobium loti

US-10-369-493-12116

Query Match 77.9%; Score 1783; DB 15; Length 452;
Best Local Similarity 77.8%; Pred. No. 8.4e-140;
Matches 351; Conservative 33; Mismatches 63; Indels 4; Gaps 2;

QY 1 MLHGASRPATARKSGSGTIRIPGDKSISHRSPFGGLASGERTITGLLEGEDVINTG 60
DB 1 MSHSACPATARKSGLTGEIRIPGDKSISHRSPFGGLASGERTITGLLEGEDVINTG 60
QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLPDFGNAATGCRITMGLVGVYDPDSTFI 120
DB 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLPDFGNAATGCRITMGLVGVYDPDSTFI 120
QY 121 GPASLTGRPMGVNPLREMGVQV-KSEDDRLPYTLRGKPTPTPTTYRVPMAAQVKSAY 179
DB 121 GPASLSKRMGVNPLREMGVQVEABEDRMPPLTIGPRITANPLAVRVPMAAQVKSAY 180
QY 180 LLAGLNTPGITTVIEPMTDHEKMLQSGANLTVETDADGVRTIRLEGKLTGQVTD 239
DB 181 LLAGLNTPGITTVIEPMTDHEKMLQSGANLTVETDADGVRTIRLEGKLTGQVTD 240
QY 240 VEGDPSSTAFPLVAALVPGSDVTILNVLNMPRTGLITLQEMGADIEVINPRLAGSD 299
DB 241 VEGDPSSTAFPLVAPLVGSEVTVIRNVLMNPTRTGLITLQEMGADIEVINPRLAGSD 300
QY 300 VADLRVRSSTLKGTVPEBRAPSMIDEPYLAFAAGATVNGLEIRVKSDELISA 359
DB 301 VADLRVRSSTLKGTVPEBRAPSMIDEPYLAFAAGATVNGLEIRVKSDELISA 360
QY 360 VANGKLKNGVDCDEGETSLVVRGPRDGKGLGNASGAATVTHDHRIRMSFLVMGLV 416
DB 361 VANGKLKNGVDCDEGETSLVVRGPRDGKGLGNASGAATVTHDHRIRMSFLVMGLV 420
QY 417 SENPYVDATMTATSPPEFMDLMAIGAKI 447
DB 421 TEKPYTIDQAMTATSPPEFMDLMAIGAKI 451

RESULT 12

US-10-369-493-20766

Sequence 20766, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

FILE REFERENCE: 38-10(52052)B

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 20766

LENGTH: 430

TYPE: PRF

ORGANISM: Rhodospseudomonas palustris

US-10-369-493-20766

Query Match 53.9%; Score 1233.5; DB 15; Length 430;
Best Local Similarity 60.0%; Pred. No. 4.5e-94;
Matches 259; Conservative 49; Mismatches 113; Indels 11; Gaps 5;

QY 9 PATARKSGSGTIRIPGDKSISHRSPFGGLASGERTITGLLEGEDVINTGKAMQAMGA 68
DB 6 PLQARKSGALHGTARVPDKSISHRALITGALAVETRIITGLLEGEDVINTKAKARALGA 65
QY 69 RIRKEGD-TWIDGVNGGLAPAPLPDFGNAATGCRITMGLVGVYDPDSTFI GPASLTGR 127
DB 66 KVERTGDCMRVHGVAGFATPEAPLPDFGNSGTICRLAMGVAGSPVATVDGASLARS 125

Qy	128	RPMGRVYNLPFREGVQ-VKSEDCDRLPVTLRGKPTPTTYRVPMSAOKVASVLLAGN	186
	126	RPKRRIYDPLMLMGAKVAVSSBGGKRLPALQGRDPLPLYRTVPVSAQIKSAVLLAGIS	185
Qy	187	TPGITTVEIEIMTRDHTKMLQGFGANLIVETADGV--RTTIRBERGKLTQOVIDP	244
Db	186	APGITTIVIEEAARDHTLMLQHFGA--TIVTBAEGNHGRKISLTQPELRGAPVVPD	243
Qy	245	PSSTAEPVLAALLVPQSDVTILNVLMNPTRTGLIILTQEWGADIEVINRLAGGEDVADL	304
Db	244	PSAAAPMVNALVVPQSDIELTDVMTNPLRTGLITTLREMGASIEDSDVRGADGEMPAF	303
Qy	305	RVPSSITKGYTVEDRAPSKMIDYPIILAAVAAPAEQATVWNGLEBLRVKESDPLSAVANG	364
Db	304	RVRGSKLKGYEVPEPERAPSMIDELYILAAVAAPAEQGTVWRGCIHEIRVYESDRLKETAAM	363
Qy	365	LKINGVDCDEGEFSLVVRGRPDGKGLGNASGAVAHLDHRIAMSLVWNGVISENPVTD	424
Db	364	LRVNGVAVLEAGDDLVIEGRGHVPG-----GGVAATHMDHRIAMSLAMGLAKDKPVTD	418
Qy	425	DATMIATSPDEF	436
Db	419	DTAFIATSPDEF	430

```

RESULT 13
US-10-369-493-10476
; Sequence 10476, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ. ID NOS: 47374
; SEQ. ID NO 10476
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Spingomonas aromaticivorans
; US-10-369-493-10476

```

Query Match	53.0%	Score 123.5	DB 15	Length 432
Similarity	59.0%	Pred. No. 2.1e-92		
Best Local				
Matches 250	Conservative 49	Mismatches 124	Indels 1	Gaps 1

QY 18 LSGTAVRIPGPKSLSHSFMFGGLASGSTRITGLLEEDVIYNKKAQCAQAGARIRKGD-T 76

Db 9 LKORIGVPGKSLSHSIMGALAVETRITGLLEEDVILSTAAANRAAGATITERADDM 68

QY 77 WIIDVGNGGLAPAEPLDFGNAAATGRLTMGLVGYVDPSDFITGDASTLTKRPMGRVLP 136

Db 69 WHHGVGVGGLLPQOALDMGNSGTSLRLMGLVAHPITATYATFVGDASLSKPMGRVIRP 128

QY 137 LREMGVGVKSEDDRLPVTLRGPKPTPIIYVRPMASAVKSVLLAAGINTGITTVEIP 196

Db 129 LSTMGAEFTASPGGRPLPTLRGISPAVPIYRPLPVAQVKSANVLAAINTGQVTVIEP 188

QY 197 IMTRDHTKMLQGFANLIVETDADGVYTRILEGRGLTGQVIDVGDPSSTAFPLVAAL 256

Db 189 IPRDHSERMLRGFGLTVDVADGARVIRVGEALPKQDIAVGDPSAAFPVVAL 248

QY 257 LVPSDVTIINLMNPRTGLIILTGEMADIVINPRLAGEVDVADLRSSSTLKGTVV 316

Db 249 LVRESDDLVENVGNTFPRALFVULIRMGGSEIELNRREVGEPVADLRHSHLLGTIDV 308

[illegible]

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RESULT 14
US-10-369-493-7814
; Sequence 7814, Application US/10369493
; Publication No. US2003023675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OR INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7814
LENGTH: 418
TYPE: PRT
; ORGANISM: Rhodobacter sphaeroides
US-10-369-493-7814

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Query Match	Score	DB	Length
51.9%	1188.5	15	418

Matches 247; Conservative 52; Mismatches 117; Indels 9; Gaps 4;

Qy	18	LSGTVIIPGKSTISHRSFMFGGLASGETRITGLBEGEDVINTKAMQAGAIRKREG-DT	76
Dd	1	LKRAETIPGKSTISHRALLIGMAVETRIITGLBEGEDVLDTRAKAMRAAGAVIQHGP	60
Qy	77	WIIDVGNGLLAPEAPLDFGNATGCRULMGLVGVYDFDSTFIGDASTIKPEMGRVILNP	136
Dd	61	MSVHGVGVGGFTPEPAVIVIDGNSGCTGVRLVMGAMATSPLTATFTGDSAIRKPMGRVTD	120
Qy	137	LREMGVQVSEDDRLPYTLRGPKPTPTITTYVPMASAVKAVYLLAGINTRGITTVIER	196
Dd	121	LALFGPAVGRKKGRIPMTLVGADVPFRVTPVPSAVKSAVLAGINAGQTVIER	180
Qy	197	INTRDTEKMLQSGFANLFTVETDADGVTIRLEGKGLGVYIDVGDSPSTAFPLVAL	256
Dd	181	EARRDSERKLRFGAELEISVETGPES-QYITTLGQELARPQVNAVRDSSAFLPCALL	239
Qy	257	LVPGSDDVTILVIMANPRTGLILITLOEMGADIEVINPRLAGEDVADLVRSSTLKGVTV	316
Dd	240	IVGSEILVPGVSRNPRTDGLVYTLLEMAGADIAFENEREGECPVADLTVRASAALKGVTV	299
Qy	317	PERABSMIDEVYILLVAAPAEAGATVMNGLBELIRKESDRLSAVANGIKLVGQDCEGE	376
Dd	300	PEPABSMIDEVYILLVAAPAEGLITTMGVLELRKESDRIDANMARGLEACGVNIEBEE	359
Qy	377	TSIIVSGRPDCKIGLNA-SGAAVATHLDRIRIAMSFLMGLVSENPVYDADATMIATISPE	435
Dd	360	DTLIVH-----GMGRVPGGATCATHLDRIRIAMSFLVIGMAABAPVYDGDGSPATISFPA	413
Qy	436	FNMDL 440	
Dd	414	FIDLM 418	


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RESULT 15
US-10-369-493-18039
; Sequence 18039, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 18039
; LENGTH: 420
; TYPE: PRT
; ORGANISM: SPHINGOMONAS
US-10-369-493-18039

Query Match      50.2%; Score 1149.5; DB 15; Length 420;
Best Local Similarity 57.1%; Pred. No. 4.3e-87;
Matches 240; Conservative 47; Mismatches 128; Indels 5; Gaps 3;

QY 18 LSGTRIPGDKSISHSFMEGGLASGETRITGLLEGEDVINTGKMQAMGARI-RKEDGT 76
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1  LRGITVTPEDKSIHSRAIFSAIAYESHEGLLEGEDVLAIAAMRAMGAEVERGEDGI 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 77 WIIDVGNGLLAPEAPLDFGNAATGCRUTMGIVGYDPDSFTIGDASITKRPGRVLNP 136
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 WRVHGIVGGLQPPAQLMGNSTSTRLMGLVASHGITATFTGDASLSGRPMGRVIEP 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 137 LREMGOVQSESDGRLPVTLRGPKTPTTYRVPMASAOYKSAVLLAGLNTPGITTVIEP 196
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 LSQMGAEITASPGRLPLMRGCPAIVPTAYTLPVASAOVKSAILLAGLNTPGITRVIEP 180
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 197 IMTRDHTKMLQGFANLFTETDADGRTIRLEGKLTGQVIDVPDPSSTAFLVVAL 256
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 181 VPTRHSEMLRGFGHELTVEDSPES-KIISVTEAEELKPQHIWPGDPSAGFMWVAAS 239
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 257 LVPGSDEVILLNVLMPNTRTGLILLTQEMGADIEVINPRLAGEDEVADLRSSSTLKGVTV 316
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 240 IVPGSEITIANVCNMPNTRTGLITALRLMGADIAETNARTVGGEPPVADLVVRHAALKALEV 299
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 317 PEDRAPSMIDEPIILAVAAAPAEAGATVMNGLEELRYKESDRLSAVANGIKLNGVDCDEGE 376
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 300 PADLAPSMIDEPVLEVAALAEGRFVARGAHELRVKESDRISTWRTALEACGVTEEP 359
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 377 TSLVVRGRPDGKGLNAGAAVATHLDRHIAVSFLVMGLVSENPVTVDDATMIATSEPEF 436
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 360 DGLAIQG---SGGAPLAGGCTVATRIIDRIIASMTVAALAAOPIAIDVAVAPATSYENP 416
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Search completed: April 20, 2005, 15:36:19
Job time : 141 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compen Ltd.

OM protein - protein search, using sw model

Run on: April 20, 2005, 15:18:11 ; Search time 44 Seconds
(without alignments)
771.939 Million cell updates/sec

Title: US-10-622-201-70
Perfect score: 2288
Sequence: 1 MLHGASRRPARKSSGLSG.....FMDLMAGLGAETLSDTRAA 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/pdata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/pdata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/pdata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/pdata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/pdata/1/1aa/PCUS_COMB.pep:*
6: /cgn2_6/pdata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2282	99.7	455	1	US-08-476-008-3
2	2282	99.7	455	1	US-08-306-063-3
3	2282	99.7	455	1	US-08-833-485-3
4	2282	99.7	455	5	US-09-137-440-3
5	2282	99.7	455	5	PCT-US91-06148A-3
6	1900.5	83.1	449	1	US-08-476-008-5
7	1900.5	83.1	449	1	US-08-306-063-5
8	1900.5	83.1	449	1	US-08-306-063-7
9	1900.5	83.1	449	1	US-08-306-063-7
10	1900.5	83.1	449	1	US-08-833-485-5
11	1900.5	83.1	449	1	US-08-833-485-7
12	1900.5	83.1	449	3	US-09-137-440-5
13	1900.5	83.1	449	3	US-09-137-440-7
14	1900.5	83.1	449	5	PCT-US91-06148A-5
15	1900.5	83.1	449	5	PCT-US91-06148A-7
16	1092	47.7	220	3	US-09-011-151-13
17	989.5	43.2	782	4	US-09-252-991A-21554
18	961.5	42.0	758	4	US-09-328-352-4521
19	902.5	39.4	773	4	US-09-540-236-3590
20	867.5	37.9	447	1	US-08-476-008-67
21	867.5	37.9	447	1	US-08-306-063-67
22	867.5	37.9	447	1	US-08-833-485-67
23	867.5	37.9	447	3	US-09-137-440-67
24	866	37.8	177	3	US-09-011-151-15
25	856	37.4	431	4	US-09-107-532A-7163
26	807.5	35.3	459	4	US-09-107-433-4297
27	806	35.2	443	1	US-08-476-008-69

28	806	35.2	443	1	US-08-306-063-69	Sequence 69, Appl
29	806	35.2	443	1	US-08-833-485-69	Sequence 69, Appl
30	806	35.2	427	4	US-09-137-440-69	Sequence 69, Appl
31	805.5	35.2	427	4	US-09-583-110-3546	Sequence 3546, Ap
32	803.5	35.1	427	2	US-09-325-881-2	Sequence 2, Appl
33	798.5	34.9	427	2	US-08-896-345-2	Sequence 2, Appl
34	798.5	34.9	427	3	US-08-476-008-42	Sequence 42, Appl
35	785	34.3	428	1	US-08-306-063-42	Sequence 42, Appl
36	785	34.3	428	1	US-08-833-485-42	Sequence 42, Appl
37	785	34.3	428	3	US-09-137-440-42	Sequence 42, Appl
38	785	34.3	428	3	US-09-137-440-42	Sequence 42, Appl
39	781.5	34.2	430	4	US-09-134-000C-4980	Sequence 4980, Ap
40	704.5	30.8	415	2	US-08-896-345-4	Sequence 4, Appl
41	704.5	30.8	415	3	US-09-226-091-4	Sequence 4, Appl
42	704.5	30.8	415	3	US-09-325-881-4	Sequence 4, Appl
43	623	27.2	436	3	US-09-134-001C-3223	Sequence 3223, Ap
44	577	25.2	430	1	US-08-476-008-44	Sequence 44, Appl
45	577	25.2	430	1	US-08-306-063-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-08-476-008-3
Sequence 3, Application US/08476008
Patent No. 5627061
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glycosylase Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,008
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6047
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
TOPOLOGY: linear

Query Match	Best Local Similarity	Score	DB 1	Length
99.7%	99.8%	2282	DB 1	455
Matches 454	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Query	1	MLHGASRPAPARSSGLSGTIVRIPGDSKISHSRSPFGSLASGERIRITGLLEGEDVINTG	60	
Db	1	MSHSAASRPAPARSSGLSGTIVRIPGDSKISHSRSPFGSLASGERIRITGLLEGEDVINTG	60	
Query	61	KAMQAMGARIRKEGDITWIIDGVNGGLAPAPAPLDFGNAATGCRITMGLVGVYDFDSTFI	120	
Db	61	KAMQAMGARIRKEGDITWIIDGVNGGLAPAPAPLDFGNAATGCRITMGLVGVYDFDSTFI	120	
Query	121	GDASLITRPMGRVILNPLREMGVQKSEDDGRLPVTLRGPKTPTPTTYVPMASQVKSAY	180	
Db	121	GDASLITRPMGRVILNPLREMGVQKSEDDGRLPVTLRGPKTPTPTTYVPMASQVKSAY	180	
Query	181	LLAALNPGITVTEPIETRTHTKMLQGFANLTVENDACGVRITRLRGGKLTGVYID	240	
Db	181	LLAALNPGITVTEPIETRTHTKMLQGFANLTVENDACGVRITRLRGGKLTGVYID	240	
Query	241	VPGPSSTAPFLVALVLPVGSDDVTILNVLNMPRTGLITLLOEMADIEVINPRLAGSD	300	
Db	241	VPGPSSTAPFLVALVLPVGSDDVTILNVLNMPRTGLITLLOEMADIEVINPRLAGSD	300	
Query	301	VADLRVRSSTLKGVTPVEDRAPSMIDEPYIIAVALAFAEGATVMNGLEELRVKESDRLSA	360	
Db	301	VADLRVRSSTLKGVTPVEDRAPSMIDEPYIIAVALAFAEGATVMNGLEELRVKESDRLSA	360	
Query	361	VANGLKINGVDCDGETSLVYRGPDGGLGNASGAALVATHDRIAMSFLVMGLVSENP	420	
Db	361	VANGLKINGVDCDGETSLVYRGPDGGLGNASGAALVATHDRIAMSFLVMGLVSENP	420	
Query	421	VTVDATMIATSPPEFMDMAGLAKIILSDTKAA	455	
Db	421	VTVDATMIATSPPEFMDMAGLAKIILSDTKAA	455	

RESULT 2

US-08-306-063-3

Sequence 3, Application US/08306063

Patent No. 5633435

GENERAL INFORMATION:

APPLICANT: Barry, Gerard F.

APPLICANT: Kishore, Ganesh M.

APPLICANT: Padgette, Stephen R.

APPLICANT: Stallings, William C.

TITLE OF INVENTION: Glycosate Tolerant

TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF

STREET: 700 Chesterfield Village Parkway

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63198

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/306,063

FILING DATE: 13-SEP-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/749,611

FILING DATE: 28-AUG-1991

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

```

1 APPLICATION NUMBER: US 07/576,537
2 FILING DATE: 31-AUG-1990
3 CLASSIFICATION: 435
4 ATTORNEY/AGENT INFORMATION:
5 NAME: Hoerner Jr., Dennis R.
6 REGISTRATION NUMBER: 30,914
7 REFERENCE/DOCKET NUMBER: 38-21 (10660)/A
8 TELECOMMUNICATION INFORMATION:
9 TELEPHONE: (314)537-6099
10 TELEFAX: (314)537-6047
11 INFORMATION FOR SEQ ID NO: 3:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 455 amino acids
14 TYPE: amino acid
15 TOPOLOGY: linear
16 MOLECULE TYPE: protein
17 US-036-063-3
18
19 Query Match 99.7%; Score 2282; DB 1; Length 455;
20 Best Local Similarity 99.8%; Pred. No. 1.9e-201;
21 Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
22
23 QY 1 MHGASRPATANKSSGSLGTVRIIPGDKISHSRSMFGGLASGETRIYTGLEGEDEVINTG 60
24 1 MSHGASRPATANKSSGSLGTVRIIPGDKISHSRSMFGGLASGETRIYTGLEGEDEVINTG 60
25
26 QY 61 KAMQAMGARIRKEGDTWIIDGVNGGILAEAPLDGMAATGCRITMGIVGVYDFDSTFI 120
27 61 KAMQAMGARIRKEGDTWIIDGVNGGILAEAPLDGMAATGCRITMGIVGVYDFDSTFI 120
28
29 QY 121 GDASLTKRPEMGRVLNPLREMGVOKSBDGRLPVTLRGPPTPIYTRVMAASQVKSAY 180
30 121 GDASLTKRPEMGRVLNPLREMGVOKSBDGRLPVTLRGPPTPIYTRVMAASQVKSAY 180
31
32 QY 181 LLAGLNTPGITTVIIEPIIMTRDHEKMLQGRGANLITVETDADGVRTIRLEGRKLTGVVID 240
33 181 LLAGLNTPGITTVIIEPIIMTRDHEKMLQGRGANLITVETDADGVRTIRLEGRKLTGVVID 240
34
35 Db 181 LLAGLNTPGITTVIIEPIIMTRDHEKMLQGRGANLITVETDADGVRTIRLEGRKLTGVVID 240
36
37 QY 241 VPDPDSSTAPPLVAALLVPGSDVTIINVLNMPRTGILITLQEMGADIEVINPLAGGED 300
38 241 VPDPDSSTAPPLVAALLVPGSDVTIINVLNMPRTGILITLQEMGADIEVINPLAGGED 300
39
40 Db 241 VPDPDSSTAPPLVAALLVPGSDVTIINVLNMPRTGILITLQEMGADIEVINPLAGGED 300
41
42 QY 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYPLIAVAAAPAGATVMNGLEELRVESDRLSA 360
43 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYPLIAVAAAPAGATVMNGLEELRVESDRLSA 360
44
45 Db 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYPLIAVAAAPAGATVMNGLEELRVESDRLSA 360
46
47 QY 361 VANGKLKLVGDCDEGETSLVVRGPPDGKGLGNASGAAVATHLDRIMSLFVNGLVSENP 420
48 361 VANGKLKLVGDCDEGETSLVVRGPPDGKGLGNASGAAVATHLDRIMSLFVNGLVSENP 420
49
50 Db 361 VANGKLKLVGDCDEGETSLVVRGPPDGKGLGNASGAAVATHLDRIMSLFVNGLVSENP 420
51
52 QY 421 VTVDATMTATSPPEFMDLMAIGAKIIEISDTYKA 455
53 421 VTVDATMTATSPPEFMDLMAIGAKIIEISDTYKA 455
54
55 Db 421 VTVDATMTATSPPEFMDLMAIGAKIIEISDTYKA 455
56
57 RESULT 3
58 US-08-833-485-3
59 ; Sequence 3, Application US/08833485
60 ; Patent No. 5804425
61 ;
62 ; GENERAL INFORMATION:
63 ; APPLICANT: Barry, Gerard F.
64 ; APPLICANT: Kishore, Ganesh M.
65 ; APPLICANT: Padgett, Stephen R.
66 ; APPLICANT: Stallings, William C.
67 ; TITLE OF INVENTION: Glycosate Tolerant
68 ; TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-phosphate Synthases
69 ; NUMBER OF SEQUENCES: 69
70 ; CORRESPONDENCE ADDRESS:
71 ; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
72 ; STREET: 700 Chesterfield Village Parkway
73 ; CITY: St. Louis
74 ; STATE: Missouri
75 ; COUNTRY: USA

```

ZIP: 63198
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/833,485
 FILING DATE: 07-APR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/306,063
 FILING DATE: 13-SEP-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/749,611
 FILING DATE: 28-AUG-1991
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/576,537
 FILING DATE: 31-AUG-1990
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Hoerner Jr., Dennis R.
 REGISTRATION NUMBER: 30,914
 REFERENCE/DOCKET NUMBER: 38-21(15117)A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314)737-6099
 TELEFAX: (314)737-6047
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 455 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-833-485-3

Query Match 99.7%; Score 2282; DB 1; Length 455;
 Best Local Similarity 99.8%; Pred. No. 1.9e-201;
 Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MLHGASRRPATARKSSGLSGTVRIPGDKSISHRSFWMFGGLASGETRITGLLEGEDVINTG 60
 1 MSHGASSRATARKSSGLSGTVRIPGDKSISHRSFWMFGGLASGETRITGLLEGEDVINTG 60
 61 KAMQAMGARIRKRGDTWIIDGVNGGLAPPAFLDFGNATGCRITMGLVGYDFDSTFI 120
 61 KAMQAMGARIRKRGDTWIIDGVNGGLAPPAFLDFGNATGCRITMGLVGYDFDSTFI 120
 121 GNASLTKRPMGRVLPRLRMGVQVKSSEDDRLPVTLRGKPTPTPIYRVPMASAOVKSAY 180
 121 GNASLTKRPMGRVLPRLRMGVQVKSSEDDRLPVTLRGKPTPTPIYRVPMASAOVKSAY 180
 181 LLAGLNTPGITTVIEIIMTRDHTKMLQGFGANLIVETDADGVRTIRLEGKLTGQVID 240
 181 LLAGLNTPGITTVIEIIMTRDHTKMLQGFGANLIVETDADGVRTIRLEGKLTGQVID 240
 241 VPQDSSTAFPLVAALLVPGSDVTIINVMNPTRTGLIITLQMGADIEVINPRLAGSD 300
 241 VPQDSSTAFPLVAALLVPGSDVTIINVMNPTRTGLIITLQMGADIEVINPRLAGSD 300
 301 VADLRKRSSTLKGVTVPEDRPSMIDEPYPLAVAAAPAGCATVMNGLLELRYKESDRLSA 360
 301 VADLRKRSSTLKGVTVPEDRPSMIDEPYPLAVAAAPAGCATVMNGLLELRYKESDRLSA 360
 361 VANGKLINGVDCDEGETSLVVRGRPDGKIGNAGGAVALTHLDRITAMGFLVWGLVSENP 420
 361 VANGKLINGVDCDEGETSLVVRGRPDGKIGNAGGAVALTHLDRITAMGFLVWGLVSENP 420
 421 VVYDDATMTATSPPEFMDLMAIGIACIEISDPTKAA 455
 421 VVYDDATMTATSPPEFMDLMAIGIACIEISDPTKAA 455
 421 VVYDDATMTATSPPEFMDLMAIGIACIEISDPTKAA 455

RESULT 4
 US-09-137-440-3
 Sequence 3, Application US/09137440
 Patent No. 6248876
 GENERAL INFORMATION:
 APPLICANT: Barry, Gerard F.
 APPLICANT: Kishore, Ganesh M.
 APPLICANT: Padgett, Stephen R.
 APPLICANT: Stallings, William C.
 TITLE OF INVENTION: Glycosate Tolerant
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. B44F
 STREET: 700 Chesterfield Village Parkway
 CITY: St. Louis
 STATE: Missouri
 COUNTRY: USA
 ZIP: 63198
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/137,440
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/833,485
 FILING DATE: 07-APR-1997
 APPLICATION NUMBER: US 08/306,063
 FILING DATE: 13-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/749,611
 FILING DATE: 28-AUG-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/576,537
 FILING DATE: 31-AUG-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Hoerner Jr., Dennis R.
 REGISTRATION NUMBER: 30,914
 REFERENCE/DOCKET NUMBER: 38-21(15117)A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314)737-6099
 TELEFAX: (314)737-6047
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 455 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-137-440-3

Query Match 99.7%; Score 2282; DB 3; Length 455;
 Best Local Similarity 99.8%; Pred. No. 1.9e-201;
 Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MLHGASRRPATARKSSGLSGTVRIPGDKSISHRSFWMFGGLASGETRITGLLEGEDVINTG 60
 1 MSHGASSRATARKSSGLSGTVRIPGDKSISHRSFWMFGGLASGETRITGLLEGEDVINTG 60
 61 KAMQAMGARIRKRGDTWIIDGVNGGLAPPAFLDFGNATGCRITMGLVGYDFDSTFI 120
 61 KAMQAMGARIRKRGDTWIIDGVNGGLAPPAFLDFGNATGCRITMGLVGYDFDSTFI 120
 121 GNASLTKRPMGRVLPRLRMGVQVKSSEDDRLPVTLRGKPTPTPIYRVPMASAOVKSAY 180
 121 GNASLTKRPMGRVLPRLRMGVQVKSSEDDRLPVTLRGKPTPTPIYRVPMASAOVKSAY 180
 181 LLAGLNTPGITTVIEIIMTRDHTKMLQGFGANLIVETDADGVRTIRLEGKLTGQVID 240
 181 LLAGLNTPGITTVIEIIMTRDHTKMLQGFGANLIVETDADGVRTIRLEGKLTGQVID 240

Db 181 LLAGNTGCTTIVPIRTHTEKMLQFGANLTVETDADGVRTIRLEGKLTGQVID 240
Qy 241 VPGDSSSTAPFLVALLVPGSDVTILNVLNMPRTGLITLQEMGADIEVINPRLAGGED 300
Db 241 VPGDSSSTAPFLVALLVPGSDVTILNVLNMPRTGLITLQEMGADIEVINPRLAGGED 300
Qy 301 VADLRVRSSTLKGVTPEDRAPSMIDEYPIILAVAAAFEGATVNNGLLEELRVKESDRISA 360
Db 301 VADLRVRSSTLKGVTPEDRAPSMIDEYPIILAVAAAFEGATVNNGLLEELRVKESDRISA 360
Qy 361 VANGKLNGVDCDEGETSLVVRGPRDGKLGNAAGAAVATHLDHRIAMSFLVMGLVSENP 420
Db 361 VANGKLNGVDCDEGETSLVVRGPRDGKLGNAAGAAVATHLDHRIAMSFLVMGLVSENP 420
Qy 421 VTVDATMIATSPPEFMDLMAGLAKIELSDTKAA 455
Db 421 VTVDATMIATSPPEFMDLMAGLAKIELSDTKAA 455

RESULT 5
PCT-US91-06148A-3
Sequence 3, Application PC/TUS9106148A
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
TITLE OF INVENTION: Glycosylase tolerant
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/06148A
FILING DATE: 19910828
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10535)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6047
TELEFAX: (314)537-6047
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-06148A-3

Query Match 99.7%; Score 2282; DB 5; Length 455;
Best Local Similarity 99.8%; Pred. No. 1.9e-201;
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLHGASSPATARKSSGLSGTRIPGDKSISHSRPFMGSLAGSPRTGLLGEDEVINTG 60
Db 1 MSHGASSPATARKSSGLSGTRIPGDKSISHSRPFMGSLAGSPRTGLLGEDEVINTG 60

Qy 61 KAMQAMGARIRKEDGTWIIDGVNGGLAPAPLDFGNAATGCRITWGLVGYVDFDSTFI 120
Db 61 KAMQAMGARIRKEDGTWIIDGVNGGLAPAPLDFGNAATGCRITWGLVGYVDFDSTFI 120
Qy 121 GDASITRKPMGRVNLPLEMGVQVKSDEGRLPTLRKPKPTPTTYVPMASQVKSAY 180
Db 121 GDASITRKPMGRVNLPLEMGVQVKSDEGRLPTLRKPKPTPTTYVPMASQVKSAY 180
Qy 181 LLAGNTPGCTTIVPIRTHTEKMLQFGANLTVETDADGVRTIRLEGKLTGQVID 240
Db 181 LLAGNTPGCTTIVPIRTHTEKMLQFGANLTVETDADGVRTIRLEGKLTGQVID 240
Qy 241 VPGDSSSTAPFLVALLVPGSDVTILNVLNMPRTGLITLQEMGADIEVINPRLAGGED 300
Db 241 VPGDSSSTAPFLVALLVPGSDVTILNVLNMPRTGLITLQEMGADIEVINPRLAGGED 300
Qy 301 VADLRVRSSTLKGVTPEDRAPSMIDEYPIILAVAAAFEGATVNNGLLEELRVKESDRISA 360
Db 301 VADLRVRSSTLKGVTPEDRAPSMIDEYPIILAVAAAFEGATVNNGLLEELRVKESDRISA 360
Qy 361 VANGKLNGVDCDEGETSLVVRGPRDGKLGNAAGAAVATHLDHRIAMSFLVMGLVSENP 420
Db 361 VANGKLNGVDCDEGETSLVVRGPRDGKLGNAAGAAVATHLDHRIAMSFLVMGLVSENP 420
Qy 421 VTVDATMIATSPPEFMDLMAGLAKIELSDTKAA 455
Db 421 VTVDATMIATSPPEFMDLMAGLAKIELSDTKAA 455

RESULT 6
US-08-476-008-5
Sequence 5, Application US/08476008
Patent No. 5627061
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glycosylase tolerant
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,008
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
TELECOMMUNICATION INFORMATION:

TELEPHONE: (314)537-6099
 TELEFAX: (314)537-6047
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 449 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-476-008-5

Query Match 83.1%; Score 1900.5; DB 1; Length 449;
 Best Local Similarity 82.9%; Pred. No. 2,4e-166;
 Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

QY 1 MLHGASSRPATARKSSGSGTVRIPGDKSISRSFMPFGLASGETRITLGEDEVINTG 60
 DB 1 MHSASPKRATARRSALTGERTIPGDKSISRSFMPFGLASGETRITLGEDEVINTG 60
 QY 61 KAMQMGARIRKRGDTWIIDVGNGLAPEAPLDGNAATGCRITMGLVGVYDFDSTFI 120
 DB 61 RAMQMGAKIRKRGDVIINGVNGCLQPEALDFGNAGTGARLTMGVGYDMKTSFI 120
 QY 121 GPASLTGRMGVNLPLRBMGVQVKSDEGDLPTLRGKRTPTPTTYRPMASQVKSAY 180
 DB 121 GPASLSKRMGVRNLPLRBMGVQVKAADGRMPLTIGKTNPTTYRPMASQVKSAY 180
 QY 181 ILAAGNTPGITTVIEPIMRDHTKMLQGFANLTVETDADGVRTIRLEGKGLTGQVID 240
 DB 181 ILAAGNTPGITTVIEPIMRDHTKMLQGFADLVEIDKQGRHRTIRIGQGLVGQTTID 240
 QY 241 VPGDPSSTAFPLVAALLVPGSDVTILNVLNPTRTGLITLQEMGADIEVINPRLAGSD 300
 DB 241 VPGDPSSTAFPLVAALLVPGSDVTIRNVLMNPTRTGLITLQEMGADIEVINARLAGSD 300
 QY 301 VADLRVRSSTLKGTVPEEDRAPSMIDEYITLVAAPAGATVANGLEELRYKESDRLSA 360
 DB 301 VADLRVRSSTLKGTVVPPERAPSMIDEYVLAIAAFAGEETVMQDLRLRYKESDRLAA 360
 QY 361 VANGKLINGVDDEGETSLVVRGPRDGKLGNAAGAAVATHLDRIRMSFLVWGLVSENP 420
 DB 361 VARGLEANGVDCTEGGMSLTVRGRPDGKLG--GGTVATHLDRIRMSFLVWGLVLAERX 417
 QY 421 VTVDATMIATSPPEFMDLMAIGAKIELS 450
 DB 418 VTVDSDNMATISFPEFMDMPGLGAKIELS 447

RESULT 7
 US-08-476-008-7
 ; Sequence 7, Application us/08476008
 ; Patent No. 5637061
 ; GENERAL INFORMATION:
 ; APPLICANT: Barry, Gerard F.
 ; APPLICANT: Kishore, Ganesh M.
 ; APPLICANT: Padgett, Stephen R.
 ; APPLICANT: Stallings, William C.
 ; TITLE OF INVENTION: Glycosate Tolerant
 ; TITLE OF SEQUENCES: 5-Etholpyruvylshikimate-3-Phosphate Synthases
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. B4F
 ; STREET: 700 Chesterfield Village Parkway
 ; CITY: St. Louis
 ; STATE: Missouri
 ; COUNTRY: USA
 ; ZIP: 63198
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/476,008

FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/306,063
 FILING DATE: 13-SEP-1994
 APPLICATION NUMBER: US 07/749,611
 FILING DATE: 28-AUG-1991
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/576,537
 FILING DATE: 31-AUG-1990
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Hoerner Jr., Dennis R.
 REGISTRATION NUMBER: 30,914
 REFERENCE/DOCKET NUMBER: 38-21(10660)A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314)537-6099
 TELEFAX: (314)537-6047
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 449 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-476-008-7

Query Match 83.1%; Score 1900.5; DB 1; Length 449;
 Best Local Similarity 82.9%; Pred. No. 2,4e-166;
 Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

QY 1 MLHGASSRPATARKSSGSGTVRIPGDKSISRSFMPFGLASGETRITLGEDEVINTG 60
 DB 1 MHSASPKRATARRSALTGERTIPGDKSISRSFMPFGLASGETRITLGEDEVINTG 60
 QY 61 KAMQMGARIRKRGDTWIIDVGNGLAPEAPLDGNAATGCRITMGLVGVYDFDSTFI 120
 DB 61 RAMQMGAKIRKRGDVIINGVNGCLQPEALDFGNAGTGARLTMGVGYDMKTSFI 120
 QY 121 GPASLTGRMGVNLPLRBMGVQVKSDEGDLPTLRGKRTPTPTTYRPMASQVKSAY 180
 DB 121 GPASLSKRMGVRNLPLRBMGVQVKAADGRMPLTIGKTNPTTYRPMASQVKSAY 180
 QY 181 ILAAGNTPGITTVIEPIMRDHTKMLQGFANLTVETDADGVRTIRLEGKGLTGQVID 240
 DB 181 ILAAGNTPGITTVIEPIMRDHTKMLQGFADLVEIDKQGRHRTIRIGQGLVGQTTID 240
 QY 241 VPGDPSSTAFPLVAALLVPGSDVTILNVLNPTRTGLITLQEMGADIEVINPRLAGSD 300
 DB 241 VPGDPSSTAFPLVAALLVPGSDVTIRNVLMNPTRTGLITLQEMGADIEVINARLAGSD 300
 QY 301 VADLRVRSSTLKGTVPEEDRAPSMIDEYITLVAAPAGATVANGLEELRYKESDRLSA 360
 DB 301 VADLRVRSSTLKGTVVPPERAPSMIDEYVLAIAAFAGEETVMQDLRLRYKESDRLAA 360
 QY 361 VANGKLINGVDDEGETSLVVRGPRDGKLGNAAGAAVATHLDRIRMSFLVWGLVSENP 420
 DB 361 VARGLEANGVDCTEGGMSLTVRGRPDGKLG--GGTVATHLDRIRMSFLVWGLVLAERX 417
 QY 421 VTVDATMIATSPPEFMDLMAIGAKIELS 450
 DB 418 VTVDSDNMATISFPEFMDMPGLGAKIELS 447

RESULT 8
 US-08-306-063-5
 ; Sequence 5, Application us/08306063
 ; Patent No. 5633435
 ; GENERAL INFORMATION:
 ; APPLICANT: Barry, Gerard F.
 ; APPLICANT: Kishore, Ganesh M.
 ; APPLICANT: Padgett, Stephen R.
 ; APPLICANT: Stallings, William C.

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/ TITLE OF INVENTION: Glyphosate Tolerant
/ TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
/ NUMBER OF SEQUENCES: 69
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
/ STREET: 700 Chesterfield Village Parkway
/ CITY: St. Louis
/ STATE: Missouri
/ COUNTRY: USA
/ ZIP: 63198
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/306,063
/ FILING DATE: 13-SEP-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/749,611
/ FILING DATE: 28-AUG-1991
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/576,537
/ FILING DATE: 31-AUG-1990
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hoerner Jr., Dennis R.
/ REGISTRATION NUMBER: 30,914
/ REFERENCE/DOCKET NUMBER: 38-21(10660)A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (314)537-6047
/ TELEFAX: (314)537-6099
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 449 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-306-063-5

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Query Match      83.1%; Score 1900.5; DB 1; Length 449;
Best Local Similarity 82.9%; Pred. No. 2.4e-166;
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

QY 1 MLHGASSRPATARKSSGSGTVIRIPGDKSISHSRSMFGGLASGETRITGLLEGEDVINTG 60
DB 1 MSHSASPRPATARRSEALTGEIRIPGDKSISHSRSMFGGLASGETRITGLLEGEDVINTG 60
QY 61 KAMQAMGARIRKRGDTWIIDGVNGGLAPAPLDFGNAAATGCRITMGLVGYDPSDSTFI 120
DB 61 RAMQAMGAKIRKEGDVWIINGVNGCLLOPEALDFGNAGTARLTMGLVGYTDMKTSFI 120
QY 121 GPASITKRPNGVNLPLREMGVQVSEDDRLPVTLRGKPTPTITTYRVPMAAQAQVKSAY 180
DB 121 GPASISKRPNGVNLPLREMGVQVSEADDRMPVTLIGKPTANPITTYRVPMAAQAQVKSAY 180
QY 181 LLAGLNTPGITTVIIEPIIMTRDHTKMLQGFANLTVETPDADGVRITRLGGRGLTGQVTD 240
DB 181 LLAGLNTPGVTVIIEPIIMTRDHTKMLQGFADLVETDKDGRHIRTIGQGLVGYQTTD 240
QY 241 VEGDPSSTAFPLVAALLVPGSDVTTILNVLNPTRTGLITLQEMGADIEVIMPRLAGSD 300
DB 241 VEGDPSSTAFPLVAALLVPGSDVTTIRNVLMNPTRTGLITLQEMGADIEVLNARLAGSD 300
QY 301 VADLVRSTLKGVTYVPEDRAPSMIDETIYLLAVAAAPAGATVWNGLEELRYKESDRLSA 360
DB 301 VADLVRASKLKGVTVPPEPARASMIIDEYVLLAASFAGETVMDGLDELRYVESDRLAA 360
QY 361 VANGKLKLVGDDDEGFTSLVVRGRPDGKGLGNAAGAAVATHLDHRIAMSFLVWGLVSENP 420
DB 361 VARGLEANGVDDCTEGEMSLTVRGRPDGKGLG--GGTVATHLDHRIAMSLVWGLAAERK 417

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QY 421 VTUDDATMIATISFPFMDLWAGLAKIELS 450
DB 418 VTUDDSNMIATISFPFMDMPLGAKIELS 447

RESULT 9
US-08-306-063-7
/ Sequence 7, Application US/08306063
/ Patent No. 5633435
/ GENERAL INFORMATION:
/ APPLICANT: Barry, Gerard F.
/ APPLICANT: Kishore, Ganesh M.
/ APPLICANT: Padgett, Stephen R.
/ APPLICANT: Stallings, William C.
/ TITLE OF INVENTION: Glyphosate Tolerant
/ TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
/ NUMBER OF SEQUENCES: 69
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
/ STREET: 700 Chesterfield Village Parkway
/ CITY: St. Louis
/ STATE: Missouri
/ COUNTRY: USA
/ ZIP: 63198
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/306,063
/ FILING DATE: 13-SEP-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/749,611
/ FILING DATE: 28-AUG-1991
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/576,537
/ FILING DATE: 31-AUG-1990
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hoerner Jr., Dennis R.
/ REGISTRATION NUMBER: 30,914
/ REFERENCE/DOCKET NUMBER: 38-21(10660)A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (314)537-6099
/ TELEFAX: (314)537-6047
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 449 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-306-063-7

Query Match      83.1%; Score 1900.5; DB 1; Length 449;
Best Local Similarity 82.9%; Pred. No. 2.4e-166;
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

QY 1 MLHGASSRPATARKSSGSGTVIRIPGDKSISHSRSMFGGLASGETRITGLLEGEDVINTG 60
DB 1 MSHSASPRPATARRSEALTGEIRIPGDKSISHSRSMFGGLASGETRITGLLEGEDVINTG 60
QY 61 KAMQAMGARIRKRGDTWIIDGVNGGLAPAPLDFGNAAATGCRITMGLVGYDPSDSTFI 120
DB 61 RAMQAMGAKIRKEGDVWIINGVNGCLLOPEALDFGNAGTARLTMGLVGYTDMKTSFI 120
QY 121 GPASITKRPNGVNLPLREMGVQVSEDDRLPVTLRGKPTPTITTYRVPMAAQAQVKSAY 180
DB 121 GPASISKRPNGVNLPLREMGVQVSEADDRMPVTLIGKPTANPITTYRVPMAAQAQVKSAY 180

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APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(15117)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6099
TELEFAX: (314)737-6047
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-485-7

Query Match 83.1%; Score 1900.5; DB 1; Length 449;
Best Local Similarity 82.9%; Pred. No. 2.4e-166;
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

QY 1 MLGASRRPATARKSSGLSGTVRIIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60
DB 1 MSHSASPRDPTARRESEALTEGIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60
QY 61 KAMQMGARIRKEGDTWIIDGVNGGLAPAPDPFGNAATGCRITMGLVGYDPDSTFI 120
DB 61 RAMQMGAKIRKEGDTWIIINGVNGCLQPEALDPFGNAGTARLTMGLVGYDMKTSFI 120
QY 121 GPASLTCKPMGRVNLPLREMGVQVSEDDRLPVTLRGPCTPTPTTYRVPMASAOVKSAY 180
DB 121 GPASLTCKPMGRVNLPLREMGVQVSEDDRLPVTLRGPCTPTPTTYRVPMASAOVKSAY 180
QY 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFANLTVETDADGVRTIRLEGKLTGOVID 240
DB 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFADLTETDKDGVRIIRITGOQKLTGOVID 240
QY 241 VPGDSSSTAFLVALLVPGSDVTILNVLNMPTRGTLITTOEMGADIEVLNARLAGGED 300
DB 241 VPGDSSSTAFLVALLVPGSDVTIRNVLNMPTRGTLITTOEMGADIEVLNARLAGGED 300
QY 301 VADLVRSSLTCKGVVPPEDRAPSMIDEPILAVAAFAEGATVMNGLEELRYKESDRISA 360
DB 301 VADLVRSSLTCKGVVPPEDRAPSMIDEPILAVAAFAEGATVMNGLEELRYKESDRISA 360
QY 361 VANGKLNGVDCDEGETSLVVRGPRDGKGLGNASGAAYATHLDRITAMSFVWGLVSENP 420
DB 361 VARGLEANGVDCDEGETSLVVRGPRDGKGLG---GGTAVATHLDRITAMSFVWGLVLAEXP 417
QY 421 VTVDATMTATSPPEFMDLMAGLAKIELS 450
DB 418 VTVDSDMTATSPPEFMDMPGLAKIELS 447

RESULT 12
US-09-137-440-5
Sequence 5, Application US/09137440
Patent No. 624876
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Scallings, William C.
TITLE OF INVENTION: Glycophosphate Tolerant
TITLE OF INVENTION: 5-Ethoxytryptophan-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF

STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/137,440
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/833,485
FILING DATE: 07-APR-1997
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(15117)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6099
TELEFAX: (314)737-6047
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-137-440-5

Query Match 83.1%; Score 1900.5; DB 3; Length 449;
Best Local Similarity 82.9%; Pred. No. 2.4e-166;
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

QY 1 MLGASRRPATARKSSGLSGTVRIIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60
DB 1 MSHSASPRDPTARRESEALTEGIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60
QY 61 KAMQMGARIRKEGDTWIIDGVNGGLAPAPDPFGNAATGCRITMGLVGYDPDSTFI 120
DB 61 RAMQMGAKIRKEGDTWIIINGVNGCLQPEALDPFGNAGTARLTMGLVGYDMKTSFI 120
QY 121 GPASLTCKPMGRVNLPLREMGVQVSEDDRLPVTLRGPCTPTPTTYRVPMASAOVKSAY 180
DB 121 GPASLTCKPMGRVNLPLREMGVQVSEDDRLPVTLRGPCTPTPTTYRVPMASAOVKSAY 180
QY 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFANLTVETDADGVRTIRLEGKLTGOVID 240
DB 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFADLTETDKDGVRIIRITGOQKLTGOVID 240
QY 241 VPGDSSSTAFLVALLVPGSDVTILNVLNMPTRGTLITTOEMGADIEVLNARLAGGED 300
DB 241 VPGDSSSTAFLVALLVPGSDVTIRNVLNMPTRGTLITTOEMGADIEVLNARLAGGED 300
QY 301 VADLVRSSLTCKGVVPPEDRAPSMIDEPILAVAAFAEGATVMNGLEELRYKESDRISA 360
DB 301 VADLVRSSLTCKGVVPPEDRAPSMIDEPILAVAAFAEGATVMNGLEELRYKESDRISA 360
QY 361 VANGKLNGVDCDEGETSLVVRGPRDGKGLGNASGAAYATHLDRITAMSFVWGLVSENP 420
DB 361 VARGLEANGVDCDEGETSLVVRGPRDGKGLG---GGTAVATHLDRITAMSFVWGLVLAEXP 417
QY 421 VTVDATMTATSPPEFMDLMAGLAKIELS 450

Db 418 VTVDSSNMIAISFPEFMDMPCGLAKIELS 447

RESULT 13

US-09-137-440-7
Sequence 7, Application US/09137440
Patent No. 6248876
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Scallings, William C.
TITLE OF INVENTION: Glycophosphate Tolerant
TITLE OF INVENTION: 5-Etholpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/137,440
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/833,485
FILING DATE: 07-APR-1997
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(15117)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6099
TELEFAX: (314)737-6047
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-137-440-7

Query Match 83.1%; Score 1900.5; DB 3; Length 449;
Best Local Similarity 82.9%; Pred. No. 2.4e-166;
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

Db 1 MSHGSSRPATRKSSGSGTIRIPGDKSISHRSMFGLAGERTITLLEGEDEVINTG 60
1 KAMQAMGARIRKRGGTWIIDVNGGLAPLPLFGNATGCRITMGLVGYDFDSFPI 120
61 RAMQAMGARIRKRGGTWIIDVNGGLAPLPLFGNATGCRITMGLVGYDFDSFPI 120
61 RAMQAMGARIRKRGGTWIIDVNGGLAPLPLFGNATGCRITMGLVGYDFDSFPI 120
QY 121 GDASTKTPMGVNLPLRMGVQVKSDDRLPVTIRGKPTPTPTTYRVPMASAOVKSAY 180
121 GDASTKTPMGVNLPLRMGVQVKSDDRLPVTIRGKPTPTPTTYRVPMASAOVKSAY 180
Db 121 GDASTKTPMGVNLPLRMGVQVKSDDRLPVTIRGKPTPTPTTYRVPMASAOVKSAY 180

QY 181 ILAGTPEGITTVIEPIIMTRDTERKLOGFANLTVETDADGVRTIRLEGKLTGOVID 240
Db 181 ILAGTPEGITTVIEPIIMTRDTERKLOGFANLTVETDADGVRTIRLEGKLTGOVID 240
QY 241 VGGDSSSTAFPLVAALLVPGSDVTLLNVTANMPTRTGLITLQEMGADIEVINPRLAGED 300
Db 241 VGGDSSSTAFPLVAALLVPGSDVTLLNVTANMPTRTGLITLQEMGADIEVINPRLAGED 300
QY 301 VADLRVRSSTLKGVTVPEDRAPSMIDEYPIILAVAAFPAGATVNMGLELRKESDRISA 360
Db 301 VADLRVRSSTLKGVTVPEDRAPSMIDEYPIILAVAAFPAGATVNMGLELRKESDRISA 360
QY 361 VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAATVHLDHRIANSFLVMGLVSENP 420
Db 361 VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAATVHLDHRIANSFLVMGLVSENP 420
QY 421 VTVDATMIATISFPEFMDMPCGLAKIELS 450
Db 421 VTVDATMIATISFPEFMDMPCGLAKIELS 450
QY 418 VTVDSSNMIAISFPEFMDMPCGLAKIELS 447
Db 418 VTVDSSNMIAISFPEFMDMPCGLAKIELS 447

RESULT 14

PCT-US91-06148A-5
Sequence 5, Application PC/TUS9106148A
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
TITLE OF INVENTION: Glycophosphate Tolerant
TITLE OF INVENTION: 5-Etholpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/06148A
FILING DATE: 19910828
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/749,611
FILING DATE: 28-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10535)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-06148A-5

Query Match 83.1%; Score 1900.5; DB 5; Length 449;
Best Local Similarity 82.9%; Pred. No. 2.4e-166;
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

Qy	1	MHGASSRPAATKSSGSLGATIRIGODSISHRSMPGGLASGETRTGLLEGEDVNTG	60
Db	1	MSHSAPKATARRSRALTGEIRIPODXSISHRSMPGGLASGETRTGLLEGEDVNTG	60
Qy	61	KAMQAMGARIKREGDWTIIDVGVNGGLLAPEAPLIDFGNAATGCRITMGLVGVDFDSTFI	120
Db	61	RAMQAMGAKIRREGDWTIINGVNGCLOLPEAALDPFGNAGTGARLTWGLVGTYDMKRSFI	120
Qy	121	GDA.SLTKRMGVYLANLRBMGVYKSSBGGDLPLPULRQPKTPTPTTYRVPAASQOVSAV	180
Db	121	GDA.SLSKRPGRVLANLRBMGVQVEADDRNP.LTLPKTRANPLTYRVPAASQOVSAV	180
Qy	181	LLAGLNTPGITVIIIEIMTRDHTKMLQGFGANLTVEVDADGVSTRILEGRGKLTGVVID	240
Db	181	LLAGLNTPGITVIIIEIVMTRDHTKMLQGFGANLTVEVDKGVHRIARTTGGKLVGCTID	240
Qy	241	VPEDBESTAFPLVYALILVPGSDVTLIANTLMNTRTGLLITLOENMADIEVINPLLAGGED	300
Db	241	VPEDBESTAFPLVYALILVPGSDVTLIRNVLNMNTRTGLLITLOENMADIEVINPLLAGGED	300
Qy	301	VADLRVRSSTLKGVTVPEBDPAPSMIDEYVILVAAPAFAGATVMNGSEELRVKESDRLSA	360
Db	301	VADLRVRASTLKGVTVPPERAPSMIDEYVILVAAPAFAGETVMDGLDELRVKESDRLAA	360
Qy	361	VANGKLKLVGDCDEGETSLVVRGRPDGKGLGNASGAAYATHLI.DHRIANSP.LVMGLVSENP	420
Db	361	VANGKLKLVGDCDEGETSM.LTVVRGRPDGKGLG---GQVATHLIDHRIANSP.LVMGLAAEKP	417
Qy	421	VTVYDDATMTATSPPEEMDMAGLGAKEI.TS	450
Db	418	VTVYDDSNMTATSPPEEMDMMPGAGAKEI.TS	447

RESULT 15
 PCT-US91-06148A-7
 Sequence 7, Application PC/TUS9106148A
 GENERAL INFORMATION:
 APPLICANT: Barry, Gerard F.
 APPLICANT: Kishore, Ganesh M.
 APPLICANT: Padgett, Stephen R.
 TITLE OF INVENTION: Glyphosate Tolerant
 TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthase
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
 STREET: 700 Chesterfield Village Parkway
 CITY: St. Louis
 STATE: Missouri
 COUNTRY: USA
 ZIP: 63198
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/06148A
 FILING DATE: 19910828
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/749,611
 FILING DATE: 28-AUG-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/576,537
 FILING DATE: 31-AUG-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Hoerner Jr., Dennis R.
 REGISTRATION NUMBER: 30,914
 REFERENCE/DOCKET NUMBER: 38-21(10535)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314)537-6099
 TELEFAX: (314)537-6047
 INFORMATION FOR SEQ ID NO: 7:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US91-06148A-7

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Query Match	83.1%;	Score 1900.5;	DB 5;	Length 449;
Best Local Similarity	82.9%;	Pred. No. 2.4e-166;		
Matches 373;	Conservative 32;	Mismatches 42;	Indels 3;	Gaps 1;

Qy	1	MLHJASSRPTTARSSGSGSVTRJPGKXKSIHSRFMFGLASGETRTJGLLEGEDEVINTG	60
Db	1	MSHSASRKPATARSEALTGEIRIRPKDKSISHRFMFGLASGETRTJGLLEGEDEVINTG	60
Qy	61	KAMQAMGARIRKEGDVIIIDGVNGGGLIAPAPLPDFGNATGCTLTMGVLGVYDPDSTFI	120
Db	61	RAMQAMAKIRKEGDVMIINGVNGCGLLOPEAALDPGNAAGTGAALTLMGLVCTYDMKTSFI	120
Qy	121	GDA\$LTRPMPGRVYNLPREMGVOYKSDGRLPYTLRGPRTPEYITRVPMA\$OVK\$AV	180
Db	121	GDASLSRPMGRVYNLPREMGVOYEAADGDBMPLTLGPKTANPITTRVPMA\$OVK\$AV	180
Qy	181	LLAGINTPGLITTVIEPIINTRDHTKMLQGFEGANLTVEITDADGVRTIRLEGRKLTGYVID	240
Db	181	LLAGINTPGVTLTIEPVWTRDHTKMLQGFEGADLTVEITDKGVYHRIITGQOKLVGQITID	240
Qy	241	VPGDPSTAPPLVVAALLVPGSDVTILLVNNPRTGTGLITLQEMGADIEVINPRLAGED	300
Db	241	VPGDPSTAPPLVVAALLVEGSDVTIRVNNPRTGTGLITLQEMGADIEVINARLAGED	300
Qy	301	VADIRVSSSTLKGTVPEDRAPSMIDEXPIIAVAAAFAGATVNNGBEELRVKESDRLSA	360
Db	301	VADIRVPA\$KLGKVVVPEPRAP\$MIDEXPIVATAI\$AFBEGSTVWDGDELKVKESDRLLA\$	360
Qy	361	VANGIKINGVDCDEGETSLVVRGRPDGKIGI\$NAGAAVATHLDRIRIAMSFLVMGI\$VENP	420
Db	361	VARGLEANGVDCETGEM\$SLTVRGRPDGKIGI\$---GGTAVATHLDRIRIAMSFLVMGI\$AAEXP	417
Qy	421	VTYVDA\$TMINT\$PEPFMDI\$MAGAKTIELS	450
Db	418	VTYVDSNNIAT\$PEPFMDM\$MGLAKTIELS	447

Search completed: April 20, 2005, 15:24:34
Job time : 51 secs

TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 7: